

2 32
CTT TCA GAA GCC CGG GAG AGC GTC TTG GGG GAT TTG CTG AAG GTT GTG CTG TAC AGC CTG
leu ser glu ala arg glu ser val leu gly asp leu leu lys val val leu tyr ser leu

62 92
GGC AGT GCC CAG AGT GCC CTC TTC TTG CAG CAT GGC CTG GCC ACC CAG AGG GCC CTT GTG
gly ser ala gln ser ala leu phe leu gln his gly leu ala thr gln arg ala leu val

122 152
TCC AAG TTC CCG GAG CTG CTG TTC GAG GAG GAC ACG GAG CTG TGT GCC GAC CTG TGC CTG
ser lys phe pro glu leu leu phe glu glu asp thr glu leu cys ala asp leu cys leu

182 212
AGG CTC CTA CGA CAC TGT GGC AGC CGC ATC AGC ACC ATC CGC ACG CAC GCC AGC GCC TCG
arg leu leu arg his cys gly ser arg ile ser thr ile arg thr his ala ser ala ser

242 272
CTG TAC CTG CTC ATG CGA CAG AAC TTC GAG ATC GGC CAC AAC TTT GCC CGT GTG AAG ATG
leu tyr leu leu met arg gln asn phe glu ile gly his asn phe ala arg val lys met

302 332
CAG GTC ACC ATG TCT CTC TCG TCC CTG GTG GGG ACG ACG CAG AAC TTC AGT GAA GAG CAC
gln val thr met ser leu ser ser leu val gly thr thr gln asn phe ser glu glu his

362 392
CTG CGA CGT TCA CTC AAA ACC ATC CTC ACC TAT GCT GAG GAG GAC ATG GGG CTG CGG GAC
leu arg arg ser leu lys thr ile leu thr tyr ala glu glu asp met gly leu arg asp

422 452
AGC ACC TTC GCA GAG CAG GTC CAG GAC CTG ATG TTC AAC CTG CAC ATG ATC CTG ACG GAC
ser thr phe ala glu gln val gln asp leu met phe asn leu his met ile leu thr asp

482 512
ACG GTG AAG ATG AAG GAA CAC CAG GAG GAG CCT GAG ATG CTC ATC GAC CTC ATG TAC AGA
thr val lys met lys glu his gln glu asp pro glu met leu ile asp leu met tyr arg

542 572
ATT GCC CGG GGC TAC CAG GGC TCA CCG GAC CTT CGG CTG ACC TGG TTG CAG AAC ATG GCC
ile ala arg gly tyr gln gly ser pro asp leu arg leu thr trp leu gln asn met ala

602 |xxxxxxxxxxxxxxx transmembrane domain xxxxxxxxxxxxxx
GGG AAG CAC GCG GAG CTG GGC AAC CAC GCC GAG GCC GCC CAG TGC ATG GTG CAC GCG GCC
gly lys his ala glu leu gly asn his ala glu ala ala gln cys met val his ala ala

xxxxxxxxxxxxxxxxxxxxxxxxxxxx| 692
 GCC CTC GTG GCT GAG TAC CTC GCC CTG CTC GAG GAC CAC CGC CAC CTG CCC GTG GGC TGC
 ala leu val ala glu tyr leu ala leu leu glu asp his arg his leu pro val gly cys

722 752
 GTT TCC TTC CAG AAC ATC TCA TCC AAT GTG CTA GAG GAG TCC GCC ATC TCC GAC GAC ATC
 val ser phe gln asn ile ser ser asn val leu glu glu ser ala ile ser asp asp ile

782 812
 CTG TCG CCC GAC GAG GAG GGC TTC TGC TCC GGG AAG CAC TTC ACT GAG CTG GGG CTG GTA
 leu ser pro asp glu glu gly phe cys ser gly lys his phe thr glu leu gly leu val

842 872
 GGG TTG CTG GAA CAG GCA GCC GGC TAC TTC ACC ATG GGC GGG CTC TAC GAG GCG GTG AAT
 gly leu leu glu gln ala ala gly tyr phe thr met gly gly leu tyr glu ala val asn

902 932
 GAG GTC TAC AAG AAC CTC ATC CCC ATC CTG GAA GCC CAC CGT GAC TAC AAG AAG CTG GCC
 glu val tyr lys asn leu ile pro ile leu glu ala his arg asp tyr lys lys leu ala

962 992
 GCG GTG CAC GGC AAA CTG CAG GAG GCC TTC ACC AAG ATC ATG CAC CAG AGT TCC GGC TGG
 ala val his gly lys leu gln glu ala phe thr lys ile met his gln ser ser gly trp

1022 |xxxxx ITAM xxxxx|1052
 GAG CGC GTG TTC GGG ACG TAT TTC CGC GTG GGC TTC TAC GGC GCC CAC TTC GGT GAC CTG
 glu arg val phe gly thr tyr phe arg val gly phe tyr gly ala his phe gly asp leu

1082 1112
 GAT GAG CAG GAG TTT GTG TAC AAG GAG CCA TCG ATC ACG AAG CTG GCA GAG ATC TCA CAC
 asp glu gln glu phe val tyr lys glu pro ser ile thr lys leu ala glu ile ser his

1142 1172
 CGG CTG GAG GAG TTC TAC ACG GAG AGA TTT GGC GAC GAC GTC GTT GAG ATT ATC AAA GAC
 arg leu glu glu phe tyr thr glu arg phe gly asp asp val val glu ile ile lys asp

1202 1232
 TCT TAC CCT GTG GAC AAG TCC AAG CTT GAC TCA CAA AAG GCC TAC ATC CAG ATC ACG TAT
 ser tyr pro val asp lys ser lys leu asp ser gln lys ala tyr ile gln ile thr tyr

1262 1292
 GTG GAA CCG TAC TTT GAT ACC TAC GAG CTC AAG GAC CGG GTG ACC TAC TTT GAC CGC AAC
 val glu pro tyr phe asp thr tyr glu leu lys asp arg val thr tyr phe asp arg asn

1322 1352
 TAT GGG CTT CGC ACA TTC CTG TTC TGC ACG CCG TTC ACG CCG GAT GGG CGC GCA CAC GGG
 tyr gly leu arg thr phe leu phe cys thr pro phe thr pro asp gly arg ala his gly

1382 1412
GAG CTG CCC GAG CAA CAC AAG CGT AAG ACG CTG CTC AGC ACC GAC CAC GCC TTC CCC TAC
glu leu pro glu gln his lys arg lys thr leu leu ser thr asp his ala phe pro tyr

1442 1472 |xxxxxxxxxxx
ATC AAG ACT CGC ATC CGT GTG TGC CAC CGG GAG GAG ACG GTG CTG ACG CCA GTG GAG GTG
ile lys thr arg ile arg val cys his arg glu glu thr val leu thr pro val glu val

xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx Coile coil 1 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
GCC ATC GAG GAC ATG CAG AAG AAG ACA CGG GAG CTG GCC TTT GCC ACC GAG CAG GAC CCA
ala ile glu asp met gln lys lys thr arg glu leu ala phe ala thr glu gln asp pro

xx|
CCA GAT GCT AAG ATG CTA CAG ATG GTG CTT CAG GGC TCT GTA GGG CCC ACC GTG AAC CAG
pro asp ala lys met leu gln met val leu gln gly ser val gly pro thr val asn gln

1622 1652
GGT CCC CTG GAG GTG GCC CAG GTG TTT TTA GCA GAG ATC CCG GAA GAC CCC AAG CTC TTC
gly pro leu glu val ala gln val phe leu ala glu ile pro glu asp pro lys leu phe

1682 1712
CGG CAT CAC AAC AAA TTG CGG CTC TGC TTC AAG GAC TTC TGC AAG AAA TGT GAG GAT GCG
arg his his asn lys leu arg leu cys phe lys asp phe cys lys lys cys glu asp ala

xx Coiled coil 2 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
CTG CGG AAA AAT AAG GCC CTG ATT GGG CCG GAC CAG AAG GAG TAC CAC CGT GAG CTG GAG
leu arg lys asn lys ala leu ile gly pro asp gln lys glu tyr his arg glu leu glu

xx|
CGC AAC TAC TGC CGC CTG CGG GAG GCT CTG CAG CCC CTG CTT ACC CAG CGC CTG CCC CAG
arg asn tyr cys arg leu arg glu ala leu gln pro leu leu thr gln arg leu pro gln

1862 1892
CTG ATG GCA CCC ACC CCA CCC GGC CTC AGG AAC TCC TTG AAC AGA GCA AGT TTC CGA AAG
leu met ala pro thr pro pro gly leu arg asn ser leu asn arg ala ser phe arg lys

1922 1952
GCA GAC CTC TGA GCC CAC AAG GAC CAA AGC TGT ACC TAG AGG AAC CAG CAC CCG GGC CTC
ala asp leu STP

1982 2012
AGC TGT CTG TGC TGC GAG GGG AGT CTG CCC TGG TGC CCA CTG GGC TGT GGG GTG ACC ACA

2042 2072
CTG TAC TTG GGG CTG GGC CCT CTG CCC CTG TGT CCC CAT CTG TGT GCA CTG ATG CTT CCT

2102 2132
CCC TTT TTT AAT TTA AAA TGG TTT TTA TAA GCA AAA AAA AAA AAA AAA

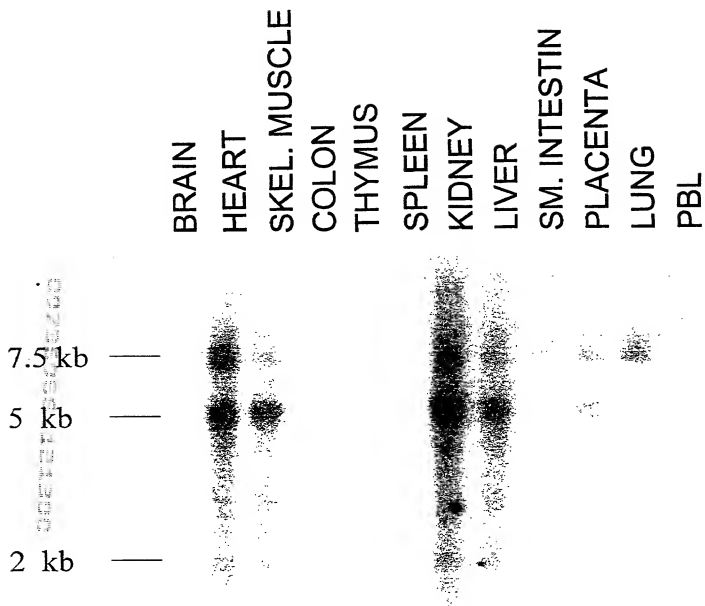


FIG. 2

HC2A
KIAA ASGNLDKNARFSAIYRQDSNKLSDNDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD
rat
HC4
HC1
HC3
HC5

HC2A
KIAA FPNYVNSSYIPTKQFETCSKTPITEFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLYDSQ
rat
HC4
HC1
HC3
HC5

HC2A
KIAA -----VLHHHQNPEFYDEIK
rat KSFARKARNIAICIEFKDSDEEDSQPLKCIYGRPGGVFTRSAFAAVLHHHQNPEFYDEIK
HC4
HC1
HC3
HC5

HC2A
KIAA IELPTQLHEKHLLLTFFHVSCDNSSKSGSTKKRDVVETQVGYSWLPPLKDGRRVVTSEQHI
rat IELPTQLHEKHLLLTFFHVSCDNSSKSGSTKKRDVVETQVGYSWLPPLKDGRRVVTSEQHI
HC4
HC1
HC3
HC5

HC2A
KIAA PVSANLP SGYLG YQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLNHFQYC
rat PVSANLP SGYLG YQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLNHFQYC
HC4
HC1
HC3
HC5 -----GPGPARSTVSI SLISNSARV

HC2A
KIAA OKTESGAQALGNELVKYLSLHAMEGHVMI AFLPTILNQLFRVLT-RATQEEVAVNVTRV
rat OKTESGAQALGNELVKYLSLHAMEGHVMI AFLPTILNQLFRVLT-RATQEEVAVNVTRV
HC4 -----MEIQVLIRFLSVILMQLFWLPMIHEDDVPISCPMV
HC1 MSFLPIILNQLFKVLV-QNEEDEITTTVTRV
HC3 NRSRSLNSNPDISGTPSPDDEVRSIIGSKGLDRSNSWVNTGGPKAAPWGSNPPSPAES
HC5

HC2A I I H V V A Q C H G L E S H L R S Y V K Y A K A E P Y V A S E Y K T V H E S T M S M T T I L K P S A D F L T S N
 KIAA I I H V V A Q C H E E G L E S H L R S Y V K Y A K A E P Y V A S E Y K T V H E E L T K S M T T I L K P S A D F L T S N
 rat
 HC4 L F H I V S K C H E E G L D S Y L S S F I K Y S F R P G K P S A P Q A P L I H E T L A T M M I A L L K Q S A D F L A I N
 HC1 L P D I V A K C H E E Q L D H S V Q S Y I K E V F K T R A C K E R F V H E D L A K N V T G L L K S N D S P T V K
 HC3 T Q A M D R S C N R M S S H T E T S S F L Q T L T G R L P T K K L F H E E L A L Q W V C S G S V R S E
 HC5 -----

Cadherin
Cleavage

HC2A K L L R Y S W F F D V L I K S M A Q H L I E N S K V K L I R N Q R F P A S Y H H A A E T V V N M L M P H I T Q K F G D
 KIAA K L L K Y S W F F D V L I K S M A Q H L I E N S K V K L I R N Q R F P A S Y H H A V E T V V N M L M P H I T Q K F R D
 rat
 HC4 K L L K Y S W F F E I I A K S M A T Y L L E E N K I K L T H G O R F P K A Y H H A L H S L F L A I T I V E S Q Y A E
 HC1 H V L K H S W F F A I I L K S M A Q H L I D T N K I Q L E R P O R F P E S Y Q N E L D N L V M V L S D H V I W K Y K D
 HC3 S A L Q Q A W F F F E L M V K S M V H H L Y F N D K L E A R K S R F P E R M D D I A L V S T I A S D I V S R F O K
 HC5 -----

HC2A N P E A S K N A N H S L A V F I K R C F T F M D R G F V F K Q I N N Y I S C F A P G D P K T L F E Y K F E F L
 KIAA N P E A S K N A N H S L A V F I K R C F T F M D R G F V F K Q I N N Y I S C F A P G D P K T L F E Y K F E F L
 rat
 HC4 I P K E S R N V N Y S L A S F L K C C L T L M D R G F V F N L I N D Y I S G F S P K D P K V L A E Y K F E F L
 HC1 A L E E T R R A T H S V A R F L K R C F T F M D R G C V F K M V N N Y I S M F S S G D L K T L C Q Y K F D F L
 HC3 D T E M V E R L I N T S L A F F L N D L L S V M D R G F V F S L I K S C Y K Q V S S K L Y S L E N P S V L V S L R L D F L
 HC5 -----

HC2A R V V C N H E H Y I P L N L F M P F G K G R I Q R Y Q D L Q L D Y S L T D E F
 KIAA R V V C N H E H Y I P L N L F M P F G K G R I Q R Y Q D L Q L D Y S L T D E F
 rat
 HC4 Q T I C N H E H Y I P L N L F M A F A K P K L Q R V Q D S N L E Y S L S D E Y
 HC1 Q E V C Q H E F I P L C L P I R S A N I P D P L T P S E S T Q E L H A S D M P E Y S V T N E F
 HC3 R I I C S H E H Y V T L N L P C S L L T P P A S P S P S V S S A T S Q S S G F S T N V Q D Q K I A M F E L S V P F
 HC5 M N A D T A P T S P C P S I S S Q N S S C S S F Q D Q K I A S M F D R S R V P A

Cadherin
EC motif

HC2A C R N H F L V G L L R E V G T A L Q E F R E V R L I A I S V L K N L L I K H S F D D R Y A S R S H Q A R I A T
 KIAA C R N H F L V G L L R E V G T A L Q E F R E V R L I A I S V L K N L L I K H S F D D R Y A S R S H Q A R I A T
 rat
 HC4 C K H H F L V G L L R E T S I A L Q D N Y E I R Y T A I S V I K N L L I K H A F D T R Y O H K N Q Q A K I A Q
 HC1 C R K H F L I G I L L R E V G F A L Q E D Q D V R H L A V L K N L M A K H S F D D R Y R E P R K Q A Q I A S
 HC3 R Q Q H Y L A G I V L T E L A V I L D P D A E G L F G L H K K V I N M V H N L L S S H D S D P R Y S D P Q I K A R V A M
 HC5 S S T S S P G L F T E L A A A L D A E G E G I S E V Q R K A V S A I H S L L S S H D L D P R C V K P E V K V K I A A

HC2A L Y L P L F G L L I E N V O R I N R D V S P F P V N A G M T V K D E S L A L P A V N P L V T P Q K G S T L D N S L H
 KIAA L Y L P L F G L L I E N V O R I N R D V S P F P V N A G M T V K D E S L A L P A V N P L V T P Q K G S T L D N S L H
 rat
 HC4 L Y L P F V G L L I E N I O R L A G R D T L Y S C A A M P N S A S R D E F P C G F T S P A N R G S L S
 HC1 L Y M P L Y G M L L D N M P R I Y L K D L Y P F T V N T S N Q G S R D D L S T N G G F Q S Q T A I K H A N S V D T S F S
 HC3 L Y L P L I G I N E T V P Q L Y D F T E T H N Q R G R P I C I A T D D Y E S E S G S M I S
 HC5 L Y L P L V G I I L D A L P Q L C D F T V A D T R Y R T S G S D E E Q E G A G A I T

HC2A KDLGAISSPYTTSTPNINSVRNADSRGSLISTDSGNSRNSEKSNLSLDKHKQSS
 KIAA KDLGAISSPYTTSTPNINSVRNADSRGSLISTDSGNSRNSEKSNLSLDKHKQSS
 rat
 HC4 TKDKTAYGSGFQNG-----HGIKREDSRGLIP-EGATGFPDQNGTGEN-----TRQS
 HC1 KDVLNSIAAFSS-----IAISTVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRL
 HC3 QTVAMAIAGTSVPQ-----LTRPGSFLITSTSGRQHT-----
 HC5 QNVALAIAGNNFN-----LKTSG-IVLSSLPYKQYN-----

HC2A TLGNSVVRCDKLDQSEIKSLMCMFLYILKMSDDALFTYWN-KASTSELMDDFTTISEVCL
 KIAA TLGNSVVRCDKLDQSEIKSLMCMFLYILKMSDDALFTYWN-KASTSELMDDFTTISEVCL
 rat
 HC4 STRSSVSQYNRLDQYEIRSLMCMFLYILKMSDDALFTYWN-KVSPQELINILILEVEL
 HC1 ALIGSTLFRDLRDLQAEIRSLMCMFLYILKMSDDALFTYWN-RAPSPVSDFFSILDLVCL
 HC3 -----TFSAESSRSLICLLWLWKN-ADETVLQKWFDTLSVLQNLRLDLLYLVCV
 HC5 -----MLNADTTRNLMICFLWIMKN-ADQSLIRKWIADLPSTQLNRILDLLFICV

HC2A HQFYQMGKRYIARNQEGLG--PIVHDRKS-----QTLPVSRNRGTMM
 KIAA HQFYQMGKRYIAR-----TGMM
 rat
 HC4 FHFYRGMKKRNIRVHDWLSKHFGIDRKS-----QTMPALRNRSGVM
 HC1 ONFRYLGGKRIIRKIAAAF--KFVQSTQNNGLTKGSNPSQTSGLLAQNMHSTRHEGHR
 HC3 SCFEYKGGKVFERNLSLTFK--KSKIMRAK-----LEEAILGSGARQEMV
 HC5 LCFEYKGGKSSDKVSTQVLQ--KSRDVKAR-----LEEALLRGEARGEMM

HC2A HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC
 KIAA HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC
 rat
 HC4 QARLQHL-----SSLESS-----FTLNHSSSTTTTADIFHQALLEGNTATEVS
 HC1 QHRSQITLPIIRGK--NALSNNPKL--LQMLDNTMTSNSNEIDIVHHVDTEANIMATEGC
 HC3 RRSRGQLERSPSGSAFGSQENLRWRKMTHTWRQNTKLDKSRAEIEHEALIDGNLATEAN
 HC5 RRRAPGNDRFP-----GLNENLRWKKEQTHWRQANEKLDKTKAELDQEALISGNLATEAH

HC2A LTALDLSLFTLAFKNQLLADHGHNPMLKKVFDVYLCLFLOKHQSETALKNVFTALRSLIY
 KIAA LTALDLSLFTLAFKNQLLADHGHNPMLKKVFDVYLCLFLOKHQSETALKNVFTALRSLIY
 rat
 HC4 -----KLSRGHSPLMKKVFDVYLCLFLOKHQSEMAKLVFTALRSLIY
 HC1 LTVLDTISFFTQCFKTHFLNNDGHNPLMKGVFDIHLAFLKNGQSEVSLKHVFAISRAFIS
 HC3 LTIILDLVSLFTQTHQRQLQCCDCQNSLMKRGFDTYMLFPQVNSQATALKHVFAISRALFVC
 HC5 LTIILDTLEIVVQTVS--VTES--KESILGGVLKVLVNSMACNQSAVYLQHCFAQORALVS
 LTIILDMQENIQASS--ALDC--KDSLLGGVLRLVNSLNCDCQSTTYLTHCFATIRALIA

HC2A KFPSTFYEGRADMCALCYEILKCCNSKLSIRTEASQLLYFLMRNFFDYTGKKSFVRTH
 KIAA KFPSTFYEGRADMCALCYEILKCCNSKLSIRTEASQLLYFLMRNFFDYTGKKSFVRTH
 rat
 HC4 KFPSTFYEGRADMCALCYEVLKCCNSKLSIRTEASQLLYFLMRNFFDYTGKKSFVRTH
 HC1 KPFAAFFKGRVNMCAAFCEYVLKCCSTKISSTRNEASALLYLMRNFFDYTKRKTFLRTH
 HC3 KPFAAFFQGPADLCSFCYEVYLKCCNHRSRSTQTEASALLYLMRKNFEFNQKQSVIRSH
 HC5 KPPELLFEEETEQCADCLRLLRHCSSSITIRSHSPASLYLLMRQNFEGN--NFARVK
 KPGDLLFEEVEEQCFDLCHQVLHHCSSMDVTRSQCACATLYLLMRFSFGATS--NFARVK

HC2A LQVIVSVSqliadvvgigetrfqqsLSIINNcANSdRLIKHTSFSSdVKDLTKRIRTVLM
 KIAA LQVIVSVSqliadvvgigetrfqqsLSIINNcANSdRLIKHTSFSSdVKDLTKRIRTVLM
 rat
 HC4 LQVIVSVSqliadvvgigetrfqqsLSIINNcANSdRLIKHTSFSSdVKDLTKRIRTVLM
 HC1 LQVIVSVSqliadvvgigetrfqqsLSIINNcANSdRLIKHTSFSSdVKDLTKRIRTVLM
 HC3 LQVIVSVSqliadvvgigetrfqqsLSIINNcANSdRLIKHTSFSSdVKDLTKRIRTVLM
 HC5 LQVIVSVSqliadvvgigetrfqqsLSIINNcANSdRLIKHTSFSSdVKDLTKRIRTVLM

Transmembrane

HC2A ATAQMKHEHNDPEMLVDLQYSLAKSYASTPELRKTLWLDMSMARIHVKNGLSEAAAMCYVHV
 KIAA ATAQMKHEHNDPEMLVDLQYSLAKSYASTPELRKTLWLDMSMARIHVKNGLSEAAAMCYVHV
 rat ATAQMKHEHNDPEMLVDLQYSLAKSYASTPELRKTLWLDMSMARIHVKNGLSEAAAMCYVHV
 HC4 ATAQMKHEHNDPEMLVDLQYSLAKSYASTPELRKTLWLDMSMARIHVKNGLSEAAAMCYVHV
 HC1 ATAQMKHEHNDPEMLVDLQYSLANSYASTPELRRTWLDSMAKIHARNGLSEAAAMCYVHI
 HC3 DTVMKHEQDPEMLIDLMYRIAGYQTSDDLRLTLQNMAGHGSERSNHAEAAQCLVHS
 HC5 DTVMKREFQDPEMLMDLMYRIAKSYQASDDLRLTLQNMAREKHTKKKQYTEAAMCLVHA

	domain	SH3	
HC2A	TALVAEYLIRKGV-----		FRQGCTAFRUITPN
KIAA	TALVAEYLIRKEA-----	VQWEPPLLPHSHSACLRRSRGGVFRQGCTAFRUITPN	
rat	TALVAEYLIRKEAD-----	LALQREPPVPFYSHTSCQRKSRGGMFRQGCTAFRUITPN	
HC4	AALVAEFLIRKKL-----		FPNGCSAFKKITPN
HC1	AALIAEYLIRKGYWKVEKIC	TASLLSEDTHPCDNSLLTTFSGGSMFSGMGPALSLITPN	
HC3	AALVAEYLSMLED-----		RKYLPGVGVTFQNISSN
HC5	AALVAEYLSMLED-----		HSYLPVGSVSFQNISSN

ITAM

HC2A IDEEASMMEDVGMQD-----VHFNEVDLMELLEQCADGLWKAERYELIADITYKLLIPI
 KIAA IDEEASMMEDVGMQD-----VHFNEVDLMELLEQCADGLWKAERYELIADITYKLLIPI
 rat IDEEASMMEDVGMQD-----VHFNEVDLMELLEQCADGLWKAERLIRAGLLTSINSSP
 HC4 IDEEAGAKEDGMMDD-----VHYSEEVLELLEQCVNGLWKAERYELISEISKLGPI
 HC1 IDEEAGAKEDSGMHD-----TPYENINLVEQLYMCGEFLWKSEHYELIADVNKPIIAV
 HC3 VLEESAVSDVVSDEEGICSGKYFTESGLVGLLEQAASFSMAGMYEAVNEVYKLLIPI
 HC5 VLEESVVSDETLSPDEGDGVCAGQYFTESGLVGLLEQAELFSTGGLYETVNEVYKLLIPI

	ITAM	ITAM	ITAM	ITAM
HC2A	YEKRRD-----			
KIAA	YEKRRDFERLAHLIDTIRHAYTSKATVEMHSGRRLGTYFRVAFFGQAQYQFTDSETDVE			
rat	SMKSGGTLETHLIDTIRHREYSKVTEVITR-----A-----AGSWDLLPGGLFGG			
HC4	YENRREFENLTQVYRTIHGAYTKILEVMHTKKRLLG-----TFFRVAFYGG			
HC1	FEKQDFKFLSLDYIDYHRSYLVKAEVNVSEKRLFG-----HYFRVAFYGG			
HC3	HEANRDAKLSTIHGKIQEAFSKIVHQSTGWERMFG-----TYFRVGFYGG			
HC5	LEAHREFRKLTLTHSKLQRAFDIVNKBH-----KRMFG-----TYFRVGFYGG			

	ITAM	ITAM
HC2A	-FFEDEDGKEYIYKEPKLTLPLSEISQRLKLYSDRFGSENVKMIQDSGKVNPKDLDSHYA	
KIAA	GFFEDEDGKEYIYKEPKLTLPLSEISQRLKLYSDRFGSENVKMIQDSGKVNPKDLDSHYA	
rat	GFFEDEDGKEYIYKEPKLTLPLSEISQRLKLYSDRFGSENVKMIQDSGKVNPKDLDSHYA	
HC4	SFFEDEDGKEYIYKEPKLTLGLSEISLRVLKLYGERFGTENVKIIQDSKVNAKELDPHYA	
HC1	GFFEEDGKEYIYKEPKLTLGLSEISQRLKLYADRFGADNVKIIQDSKNVNEKPLDPHYA	
HC3	TKFGDLDEQEFVYKEPAITKLAEISHRLEGFYGERFGEDVVEVIKDSNPVDKCKLDPNKA	
HC5	SKFGDLDEQEFVYKEPAITKLPEISHRLEAFYGGFGAEFVEVIKDSNTPVDKTKLDPNKA	

ITAM

HC2A YIDVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVVEEQCKRRTILTA
 KIAA YIDVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVVEEQCKRRTILTA
 rat YIDVTHVIPFFDEKELQERKTEFERNIRRFMFEMPFTQTGKRQGGVVEEQCKRRTILTA
 HC4 YIDVTHVYKYPFDDKELTERKTEFERNHNIISRFVEAPYTLGSKKGQGCIEEQCKRRTILTT
 HC1 YIDVTHVYVTFPEEKEIEDRKTFEMHHNINIRRFVFTPTLSGKKHGGVAAEQCKRRTILTT
 HC3 YIQITVYVEPYFDTYEMKDRITYFDKNYNLRRFMYCTPFTLDGRAHGLEHQFQRKTILTT
 HC5 YIQITVFEVYFDEYEMKDRVITYFEKNFNLRRFMYTPTFTLEGRPRGLEHQYRRNTVLTT

Coiled-Coil 1

HC2A	IHCFFPVKKRIPVMYQHHTDLNR	I	EVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQSV
KIAA	IHCFFPVKKRIPVMYQHHTDLNR	I	EVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQSV
rat	IHCFFPVKKRIPVMYQHHTDLNR	I	EVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQSV
HC4	SNSFFPVKKRIPINCEQQINLKH	I	DGATDEIKDKTAELOKLCSSTDVDMISLQLKLQSV
HC1	SHLFFPVKKRIQVISQSSSTELNRI	I	EVAIDEMSKRVSELNQLCTMEEVDMISLQLKLQSV
HC3	SHAFFPIKTRVNVTHKEEIIILTR	I	EVAIDEMQKKKTQELAFATHQDPADPKMLQVLOQSV
HC5	MHAFFPIKTRISVIQKEEFVLTR	I	EVAIDEMKKKTLQLAVAINQEPDPAKMLQVLOQSV

Coiled-Coil 2

HC2A	SVQVNAGPLAYARAFLDDTNTKRYPD	NKVKLLKEVFRQFVEACGQ	LAVNERLIKEDQLE
KIAA	SVQVNAGPLAYARAFLDDTNTKRYPD	NKVKLLKEVFRQFVEACGQ	LAVNERLIKEDQLE
rat	SVQVNAGPLAYARAFLDDTNTKRYPD	NKVKLLKEVFRQFVEACGQ	LAVNERLIKEDQLE
HC4	SVQVNAGPLAYARAFLNDSQASKYPP	PKVSELKDMFRKFIQACSI	LELNERLIKEDQVE
HC1	SVKVNAGPMAYARAFLLEETNAKKYPD	NQVKLLKEIFRQFADACGQ	LDVNERLIKEDQLE
HC3	GTTVNQGPLEVAQVFLSEIPSDPKL	FRHNNKLRLCFKDFTKRCED	FLRKNKSLIGPVQKE
HC5	GATVNGQPLEVAQVFLAEIPADPKLY	FRHNNKLRLCFKEFIMRCGE	FEVKNKRLITADQRE

Coiled-Coil 2

HC2A	YQEEMKANYREMAKELSEIMHE	QICPLEEKTSS-VLPNSLHIFNAISGTP	PTSTMVHGMTSS
KIAA	YQEEMKANYREMAKELSEIMHE	QLG-----	
rat	YQEEMKANYREIRKELSDIIVR	RICPGEDKRAKTFPAHLQRHQ	RDTNKHSGSRVDQFELS
HC4	YHEGLKSNFRDMVKELSDIIEH	QILQEDTMHSPWMSNTLHVCAISG	TSSDRGYGSPRYA
HC1	YQEELRSHYKMDLSELSTVMNE	QITGRDDLK----	RGVDQTCTRVISKATPALPTVISISS
HC3	YQRELG----	KLSS-----	PZ-----
HC5	YQQLKKNNYKLNLRPMIER	KIPELYKPIFRVSESQKRDSFHRSS	FRKCTQLSQGSZ-

PRM

SSVV-----

HC2A	CVTLPEPHVGTCTFVMCKLRTTFRAN	HWFCQAEAMNGREKEPWTVIFNSR	FYRSWGK
KIAA	EVZ-----		
rat	SAEVZ-----		
HC4	-----		
HC1	-----		
HC3	-----		
HC5	-----		

HC2A	-----
KIAA	-----
rat	VHIF
HC4	-----
HC1	-----
HC3	-----
HC5	-----

A

CLASP-1 YRVAFYGO:::GFFEEEGKEYIYKEP
 KIAA1058 FRVAFYGOAAQYQFTCSETDVEGPFEDDGKEYIYKEP
 CLASP-2 FEDEDGKEYIYKEP
 CLASP-6 FRVAFYGO:::GFFEEEGKEYIYKEP
 CLASP-4 FRVAFYGO:::SFEEEGKEYIYKEP
 DOCK180 FAVGYGQ:::GFPTFLRGKVFIYRGKEYERRERD
 DOCK2 FAVGYGQ:::GFPSFLRNKVFIYRGKEYERRERD
 DOCK3 FRVGFGYGR:::KFPFFLRNKEYVCRGH
 KIAA0716 FRVGFGYGR:::KFPFFLRNKEYVCRGH
 CLASP-3 FRVGFGYGT:::KFGDLDEQEFVYKEP
 CONSENSUS F V FYG KEY R
 YF Q F R

C

TRG PKLTPLSEISORLLKLYSDKFGSENVKMIQDSGKVNPKDLDSKFAYIQVTHVTPFFDEKE
 CLASP-1 PKLTGLSEISORLLKLYADKFGADNVKIIQDSNKNVNPDKLDPKYAIQVTVYTPFFEEKE
 CLASP-2 PKLTPLSEISORLLKLYSDKFGSENVKMTQDSGKVNPKDLDSKYAIQVTHVTPFFDEKE
 CLASP-4 PKLTGLSEISORLLKLYGKFGTENVKIIQDSNKNVNAKELDPKYAIQVTVYKPYFDDKE
 CLASP-3 PAITKLAEISHRLEGFYGERFGEDVVEVIKDSNPVDCKLDPNKAYIQITYVEPYFDTYE
 KIAA0716 HDYERLEAFQQRMLNEFPFAIA-----MOHANQPDETIFQAEAKLQIYAVTPIPESQE
 DOCK3 HDYERLEAFQQRMLSEFPQAVA-----MOHPNHPDDAILQCDAQKLIQIYAVTPIPDKVD
 DOCK2 FQMQLMTQFPNAEK-----MNTTTSAPGDDVKNAPGQYIQCFVTQPVLDDEHP
 DOCK180 EYERREDFQMQLMTQFPNAEK-----MNTTTSAPGDDVKNAPGQYIQCFVTQPVLDDEHP
 CONSENSUS L L Y YIQ+ V P D
 M F L E

D

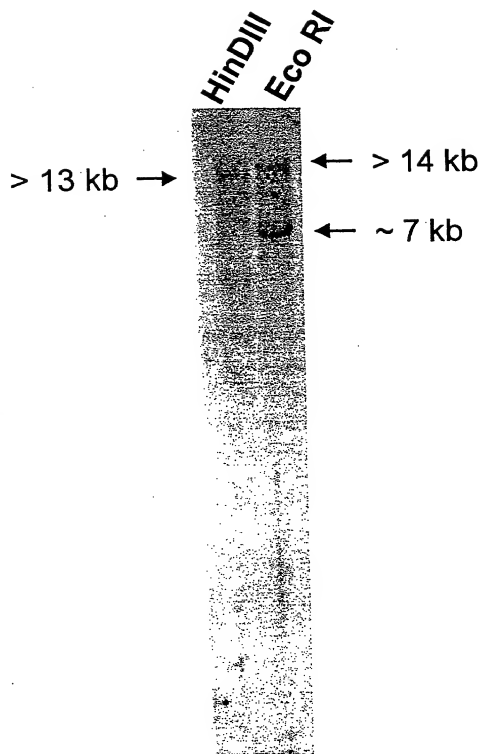
CLASP-1 RTILTTSHLFPYVKKRIQVISQSSTELNPIEVAIDEMSRKVSELN
 TRG RTILTTAIHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELR
 KIAA1058 RTILTTAIHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELR
 CLASP-2 RTILTTAIHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELR
 CLASP-6 RTILTTAIHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELR
 CLASP-4 RTILTTSHLFPYVKKRIPINCEQQINLKPIDVATDEIKDKTAELO
 CLASP-3 KTIILTTSHLFPYVKKRIPINCEQQINLKPIDVATDEIKDKTAELO
 CLASP-5 NTVLITTMHAFPYIKTRISVIOKEEFVLTPIEVAIDEMKKKTLQLA
 KIAA0716 RTSLYLVLQSLPGISRWFEVEKREVEMSPLENAIEVLNKNQQLK
 DOCK2 RTSFVTAYKLPGLIRWFEVVMHSQTTISPLENAIETMSTANEKIL
 DOCK3 RTILTTSHLFPYVKKRIPINCEQQINLKPIDVATDEIKDKTAELO
 DOCK180 RTSFVTAYKLPGLIRWFEVVMHSQTTISPLENAIETMSTANEKIL
 CONSENSUS RT L FP V + V + P+E AI+ M +L
 F L L + + + I

B

FIG. 3
 1 of 2

	F										G															
CLASP-1	SEQLKLGSVSVYVNA										SPMAYARAFLEETNAKKYFONQV--KILKEIFRQFADACGQALD															
TRG	ETOLKLGSVSVQVNA										PLAYARAFLDDINTKRYEDNKV--KILKEVFRQFVEACGQALA															
KIAA1055	KLQKLQGSVSVQVNA										PLAYARAFLDDINTKRYEDNKV--KILKEVFRQFVEACGQALA															
CLASP-2	KLQKLQGSVSVQVNA										PLAYARAFLDDINTKRYEDNKV--KILKEVFRQFVEACGQALA															
CLASP-6	KLQKLQGSVSVQVNA										PLAYARAFLDDINTKRYEDNKV--KILKEVFRQFVEACGQALA															
CLASP-3	MLQMLQGSVSGTTVNA										GLEVAQVFLSE--IPSDPKLFRHHNKLRLCFKDFTKRCEDALR															
CLASP-4	QLQKLQGCVSVQVNA										PLAYARAFLNDSQASKYPPKKVSELKDMFRKFI--QACSIALE															
CLASP-5	MLQMLQGSVSGATVNA										GLEVAQVFLAE--IPADPKLYRHHNKLRLCFKEFIMRCGEAVE															
KIAA0716	PLTMCLNGVIDAAVNGG										VSRYQEAFVKEYILSHPEEDGEKIAFLRELMLEQAQILEFGLA															
DOCK2	PLSMLLNGVIDPAVMGG										FAKYEKAFTEEYVRDHPEDQDKLTHLKDLIAWQIPFLGAGIK															
DOCK3	LLSMCLNGVIDPAVMGG										IARKQEAFDDKYINKHPGDAEKITCKELMQEQVHVLGVGLA															
DOCK180	PLSMLLNGVIDPAVMGG										FAKYEKAFTEEYVRDHPAHEKIEKLDLIAWQIPFLAEGIR															
CONSENSUS	L	M	L+G	V	VN	G	Y	AFL	+	+	P	L+	L	L	M	L+G	V	VN	G	Y	AFL	+	+	P	L+	L
	L			I			V	V	F	+			I	L			I			V	V	F	+			I

DOCK1=KIAA0269
 DOCK3=KIAA0299
 CLASPvariant=KIAA1055



genomic DNA

FIG. 4

-12 -1
GACGCGAGGACC

1/1 31/11
ATG GCT GCC TCC GAG CGC CGC GCC TTC GCG CAC AAG ATC AAC AGG ACG GTG GCC GCA GAG
Met ala ala ser glu arg arg ala phe ala his lys ile asn arg thr val ala ala glu
61/21 91/31
GTG CGG AAG CAG GTG TCC CGG GAA CGC AGT GGC TCC CCC CAC TCC AGC AGG CGC TGC AGC
val arg lys gln val ser arg arg glu arg ser gly ser pro his ser ser arg arg cys ser
121/41 151/51
AGC TCC CTG GGG GTC CCA CTG ACT GAA GTT GTC GAG CCC CTG GAC TTT GAG GAT GTA CTT
ser ser leu gly val pro leu thr glu val val glu pro leu asp phe glu asp val leu
181/61 211/71
CTG AGC CGG CCA CCA GAT GCT GAG CCC GGG CCC CTC AGG GAC CTG GTA GAA TTC CCA GCT
leu ser arg pro pro asp ala glu pro gly pro leu arg asp leu val glu phe pro ala
241/81 271/91
GAT GAC TTG GAG CTG CTG CTG CAG CCC CGG GAA TGC CGG ACC ACG GAG CCC GGG ATC CCC
asp asp leu glu leu leu leu gln pro arg glu cys arg thr thr glu pro gly ile pro
301/101 331/111
AAG GAT GAA AAA CTG GAT GCC CAG GTG AGG GCC GCG GTG GAG ATG TAT ATT GAG GAC TGG
lys asp glu lys leu asp ala gln val arg ala ala val glu met tyr ile glu asp trp
361/121 391/131
GTC ATT GTC CAC AGA AGG TAT CAG TAC CTG AGT GCA GCA TAC AGC CCC GTC ACC ACA GAC
val ile val his arg arg tyr gln tyr leu ser ala ala val glu pro val thr thr asp
421/141 451/151
ACA CAG CGG GAG CGA CAG AAG GGC CTC CCC CGC CAG GTC TTT GAG CAG GAT GCT TCT GGA
thr gln arg glu arg gln lys gly leu pro arg gln val phe glu gln asp ala ser gly
481/161 511/171
GAC GAG AGG TCC GGC CCT GAG GAC TCG AAT GAC TCC CGG CGT GGC TCG GGC TCC CCG GAA
asp glu arg ser gly pro glu asp ser asn asp ser arg arg gly ser gly ser pro glu
541/181 571/191
GAC ACC CCT CGA AGC AGT GGT GCC TCT AGC ATC TTC GAC CTG AGG AAC CTG GCA GCT GAC
asp thr pro arg ser ser gly ala ser ser ile phe asp leu arg asn leu ala ala asp
601/201 631/211
TCA TTG CTG CCC TCT CTG CTA GAG CGG GCG GCC CCA GAA GAT GTG GAC CGG CGC AAT GAA
ser leu leu pro ser leu leu glu arg ala ala pro glu asp val asp arg arg asn glu
661/221 691/231
ACC CTT CGA CGG CAG CAC CGG CCC CCG GCC CTG CTC ACC CTC TAC CCG GCA CCT GAC GAG
thr leu arg arg gln his arg pro pro ala leu leu thr leu tyr pro ala pro asp glu
721/241 751/251
GAT GAA GCC GTG GAA CGC TGT AGC CGC CCA GAG CCA CCC CGC GAG CAC TTT GGA CAA AGG
asp glu ala val glu arg cys ser arg pro glu pro pro arg glu his phe gly gln arg
781/261 811/271
ATC TTG GTC AAG TGT CTG TCG CTC AAG TTC GAG ATT GAA ATT GAG CCC ATC TTT GGG ATC
ile leu val lys cys leu ser leu lys phe glu ile glu ile glu pro ile phe gly ile
841/281 871/291
TTG GCT CTG TAT GAT GTG CGG GAG AAA AAG AAG ATC TCG GAG AAC TTC TAC TTC GAC CTG
leu ala leu tyr asp val arg glu lys lys lys ile ser glu asn phe tyr phe asp leu
901/301 931/311
AAC TCG GAC TCC ATG AAG GGG CTG CTT CGG GCT CAT GGC ACC CAC CCT GCC ATC TCC ACC
asn ser asp ser met lys gly leu leu arg ala his gly thr his pro ala ile ser thr
961/321 991/331
CTG GCC CGC TCT GCC ATC TTC TCT GTG ACC TAC CCC TCA CCT GAC ATC TTC CTG GTC ATC
leu ala arg ser ala ile phe ser val thr tyr pro ser pro asp ile phe leu val ile
1021/341 1051/351
AAG TTG GAG AAG GTG CTT CAG CAA GGG GAC ATC AGT GAG TGC TGT GAG CCT TAC ATG GTG
lys leu glu lys val leu gln gln gly asp ile ser glu cys cys glu pro tyr met val
1081/361 1111/371

TTG AAA GAA GTG GAC ACA GCC AAG AAC AAA GAG AAG CTA GAG AAG CTG CGC CTG GCG GCC
 leu lys glu val asp thr ala lys asn lys glu lys leu glu lys leu arg leu ala ala
 1141/381
 GAG CAG TTC TGC ACC CGC CTG GGC CGC TAC CGC ATG CCC TTC GCC TGG ACG GCC GTG CAC
 glu gln phe cys thr arg leu gly arg tyr arg met pro phe ala trp thr ala val his
 1201/401
 TTG GCC AAC ATC GTG AGC AGC GCT GGG CAG CTG GAC CGG GAC TCT GAC TCG GAG GGC GAG
 leu ala asn ile val ser ser ala gly gln leu asp arg asp ser asp ser glu gly glu
 1261/421
 CGC CGG CCA GCC TGG ACA GAC CGC CGC CGT CGG GGG CCC CAG GAC CGG GCG AGT AGT GGG
 arg arg pro ala trp thr asp arg arg arg arg gly pro gln asp arg ala ser ser gly
 1321/441
 GAC GAC GCC TGC AGC TTC TCT GGC TTC CGT CCA GCC ACG CTA ACT GTC ACA AAC TTC TTT
 asp asp ala cys ser phe ser gly phe arg pro ala thr leu thr val thr asn phe phe
 1381/461
 AAG CAG GAG GCT GAG CGA CTC AGT GAC GAG GAC CTC TTC AAG TTC CTG GCT GAC ATG AGG
 lys gln glu ala glu arg leu ser asp glu asp leu phe lys phe leu ala asp met arg
 1441/481
 CGC CCG TCG TCC CTG CTG CGG CGA CTA CGT CCT GTG ACT GCC CAG CTC AAG ATC GAC ATT
 arg pro ser ser leu leu arg arg leu arg pro val thr ala gln leu lys ile asp ile
 1501/501
 TCT CCG GCT CCT GAA AAT CCC CAC TTC TGC CTC TCC CCT GAG CTG CTT CAT ATC AAG CCC
 ser pro ala pro glu asn pro his phe cys leu ser pro glu leu his ile lys pro
 1561/521
 TAC CCG GAC CCC AGG GGC CGG CCC ACC AAG GAG ATT CTG GAG TTC CCC GCC CGC GAA GTC
 tyr pro asp pro arg gly arg pro thr lys glu ile leu glu phe pro ala arg glu val
 1621/541
 TAT GCC CCC CAT ACC AGC TAC AGG AAC CTG CTG TAC GTG TAC CCG CAC AGC CTC AAC TTC
 tyr ala pro his thr ser tyr arg asn leu leu tyr val tyr pro his ser leu asn phe
 1681/561
 AGC AGC CGC CAG GGC TCC GTG CGC AAC CTT GCT GTG CGA GTG CAG TAC ATG ACA GGC GAG
 ser ser arg gln gly ser val arg asn leu ala val arg val gln tyr met thr gly glu
 1741/581
 GAC CCC AGC CAG GCT CTG CCG GTC ATC TTT GGC AAG TCC AGC TGC AGT GAA TTT ACC CGC
 asp pro ser gln ala leu pro val ile phe gly lys ser ser cys ser glu phe thr arg
 1801/601
 GAG GCC TTC ACA CCG GTG GTC TAC CAT AAC AAG TCC CCC GAG TTC TAC GAG GAG TTC AAG
 glu ala phe thr pro val val tyr his asn lys ser pro glu phe tyr glu glu phe lys
 1861/621
 CTG CAT CTT CCA GCC TGC GTG ACA GAG AAC CAT CAC CTG CTG TTC ACC TTC TAC CAT GTC
 leu his leu pro ala cys val thr glu asn his his leu leu phe thr phe tyr his val
 1921/641
 AGC TGC CAG CCC CGG CCG GGC ACT GCC CTG GAG ACA CCC GTG GGC TTT ACT TGG ATC CCA
 ser cys gln pro arg pro gly thr ala leu glu thr pro val gly phe thr trp ile pro
 1981/661
 CTG CTG CAG CAC GGC CGC CTG AGG ACC GGC CCC TTC TGT CTC CCA GTG TCT GTG GAC CAG
 leu leu gln his gly arg leu arg thr gly pro phe cys leu pro val ser val asp gln
 2041/681
 CCG CCG CCC AGC TAT TCC GTG CTC ACA CCC GAT GTG GCG CTT CCG GGC ATG CGC TGG GTG
 pro pro pro ser tyr ser val leu thr pro asp val ala leu pro gly met arg trp val
 2101/701
 GAC GGT CAC AAG GGC GTG TTC AGT GTG GAG CTC ACA GCC GTG TCC TCT GTG CAC CCC CAG
 asp gly his lys gly val phe ser val glu leu thr ala val ser ser val his pro gln
 2161/721
 GAC CCC TAC CTG GAC AAA TTC TTC ACC CTG GTG CAC GTC CTG GAG GAG GGA GCC TTC CCA
 asp pro tyr leu asp lys phe phe thr leu val his val leu glu glu gly ala phe pro
 2221/741
 TTC CCG CTC AAG GAC ACT GTG CTG AGC GAG GGC AAC GTG GAG CAG GAG CTG CGG GCC AGT
 phe arg leu lys asp thr val leu ser glu gly asn val glu gln glu leu arg ala ser
 2281/761
 CTT GCA GCA CTG CGC CTG GCC AGC CCC GAA CCC CTT GTG GCC TTC TCC CAC CAC GTG CTG

leu ala ala leu arg leu ala ser pro glu pro leu val ala phe ser his his val leu
 2341/781 2371/791
 GAC AAG CTC GTG CGT CTG GTC ATC AGG CCC CCG ATC ATC AGT GGC CAG ATT GTG AAC CTG
 asp lys leu val arg leu val ile arg pro pro ile ile ser gly gln ile val asn leu
 2401/801 2431/811
 GGC CGT GGA GCC TTT GAA GCA ATG GCC CAT GTA GTC AGC CTT GTT CAC CGG AGC CTG GAG
 gly arg gly ala phe glu ala met ala his val val ser leu val his arg ser leu ala glu
 2461/821 2491/831
 GCA GCC CAG GAT GCC CGC GGT CAC TGC CCA CAG CTG GCT GCC TAC GTC CAC TAC GCC TTT
 ala ala gln asp ala arg gly his cys pro gln leu ala ala tyr val his tyr ala phe
 2521/841 2551/851
 CGC CTT CCT GGC ACT GAG CCC AGC CTC CCG GAT GGG GCC CCT CCA GTG ACA GTG CAG GCT
 arg leu pro gly thr glu pro ser leu pro asp gly ala pro pro val thr val gln ala
 2581/861 2611/871
 GCC ACA CTG GCC CGT GGC TCT GGT CGC CCC GCA AGC CTC TAC CTG GCG CGT TCC AAG AGC
 ala thr leu ala arg gly ser gly arg pro ala ser leu tyr leu ala arg ser lys ser
 2641/881 2671/891
 ATC AGC AGC AGC AAC CCT GAC CTC GCC GTG GCC CCT GGC TCT GTG GAT GAC GAG GTT TCC
 ile ser ser ser asn pro asp leu ala val ala pro gly ser val asp asp glu val ser
 2701/901 2731/911
 CGC ATC CTG GCC AGC AAG CTG CTT CAC GAG GAG CTG GCT CTG CAG TGG GTG GTC AGC AGC
 arg ile leu ala ser lys leu leu his glu glu leu ala leu gln trp val val ser ser
 2761/921 2791/931
 AGT GCC GTA CGC GAG GCC ATC CTC CAG CAC GCC TGG TTC TTC TAC CAG CTC ATG GTG AAG
 ser ala val arg glu ala ile leu gln his ala trp phe phe phe gln leu met val lys
 2821/941 2851/951
 AGT ATG GCG CTG CAC CTG CTG CTT GGC CAG CGA CTA GAC ACA CCC CGC AAG CTG CGC TTC
 ser met ala leu his leu leu leu gly gln arg leu asp thr pro arg lys leu arg phe
 2881/961 2911/971
 CCC GGA CGC TTC CTG GAC GAC ATC ACT GCC TTG GTG GGC TCT GTG GGC CTG GAG GTC ATC
 pep gly arg phe leu asp asp ile thr ala leu val gly ser val gly leu glu val ile
 2941/981 2971/991
 ACC CGT GTC CAC AAG GAT GTG GAG CTG GCC GAG CAC CTC AAC GCC AGC CTG GCT TTC TTC
 thr arg val his lys asp val glu leu ala glu his leu asn ala ser leu ala phe phe
 3001/1001 3031/1011
 CTC AGT GAC CTT CTG TCC CTG GTG GAC CGG GGC TTT GTC TTC AGC CTG GTC CGG GCC CAC
 leu ser asp leu leu ser leu val asp arg gly phe val phe ser leu val arg ala his
 3061/1021 3091/1031
 TAC AAG CAG GTG GCC ACG CGG CTC CAG TCG TCC CCT AAT CCA GCA GCC CTG CTG ACC CTG
 tyr lys gln val ala thr arg leu gln ser ser pro asn pro ala ala leu thr leu
 3121/1041 3151/1051
 CGC ATG GAA TTC ACC CGC ATC CTG TGC AGC CAC GAG CAC TAC GTG ACC CTC AAC CTC CCC
 arg met glu phe thr arg ile leu cys ser his glu his tyr val thr leu asn leu pro
 3181/1061 3211/1071
 TGC TGC CCC CTG TCA CCT CCA GCC TCG CCC TCC CCC TCT GTG TCC TCC ACC ACC TCC CAG
 cys cys pro leu ser pro pro ala ser pro ser pro ser val ser ser thr thr ser gln
 3241/1081 3271/1091
 AGC TCC ACC TTC TCC AGC CAA GCC CCG GAC CCC AAG GTG ACC AGC ATG TTC GAA CTG AGT
 ser ser thr phe ser ser gln ala pro asp pro lys val thr ser met phe glu leu ser
 3301/1101 3331/1111
 GGA CCA TTC CGG CAG CAG CAC TTC CTA GCT GGG CTC CTG CTG ACG GAG CTG GCA CTG GCC
 gly pro phe arg gln gln his phe leu ala gly leu leu leu thr glu leu ala leu ala
 3361/1121 3391/1131
 CTC GAA CCT GAG GCT GAA GGG GCA TTC CTG TTG CAC AAG AAG GCC ATC AGT GCT GTG CAC
 leu glu pro glu ala glu gly ala phe leu leu his lys lys ala ile ser ala val his
 3421/1141 3451/1151
 AGC CTG CTA TGT GGC CAT GAC ACT GAC CCC CGC TAC GCC GAG GCC ACT GTG AAG GCT CGT
 ser leu leu cys gly his asp thr asp pro arg tyr ala glu ala thr val lys ala arg
 3481/1161 3511/1171
 GTG GCC GAG CTG TAC CTG CCA CTG CTT TCG ATT GCA CGG GAT ACC TTG CCA CGG CTG CAT
 val ala glu leu tyr leu pro leu leu ser ile ala arg asp thr leu pro arg leu his

3541/1181
GAC TTT GCT GAG GGC CCA GGT CAG CGG TCA AGA CTG GCC TCA ATG CTT GAC TCA GAC ACA
asp phe ala glu gly pro gly gln arg ser arg leu ala ser met leu asp ser asp thr
3601/1201
GAA GGC GAA GGG GAC ATT GCG GGT ACC ATC AAC CCC TCT GTG GCC ATG GCC ATT GCT GGT
glu gly glu gly asp ile ala gly thr ile asn pro ser val ala met ala ile ala gly
3661/1221
GGC CCC CTA GCC CCT GGC TCC CGG GCC AGC ATC TCC CAG GGG CCA CCA ACG GCT TCT CGC
gly pro leu ala pro gly ser arg ala ser ile ser gln gly pro pro thr ala ser arg
3721/1241
GCA GGC TGT GCC CTC TCT GCT GAG TCA AGC CGG ACC TTG CTG GCG TGT GTG CTG TGG GTG
ala gly cys ala leu ser ala glu ser ser arg thr leu leu ala cys val leu trp val
3781/1261
CTG AAA AAC ACC GAG CCG GCG CTC CTG CAG CGC TGG GCC ACT GAC CTG ACA CTC CCC CAG
leu lys asn thr glu pro ala leu leu gln arg trp ala thr asp leu thr leu pro gln
3841/1281
CTG GGA CGT CTG TTG GAC TTG CTG TAC CTT TGC CTG GCT GCC TTT GAG TAC AAG GGG AAA
leu gly arg leu leu asp leu leu tyr leu cys leu ala ala phe glu tyr lys gly lys
3901/1301
AAG GCC TTT GAA CGC ATC AAC AGC CTC ACA TTC AAA AAA TCT CTG GAT ATG AAG GCG CGG
lys ala phe glu arg ile asn ser leu thr phe lys lys ser leu asp met lys ala arg
3961/1321
CTA GAG GAA GCC ATT CTG GGT ACC ATC GGA GCT CGA CAA GAA ATG GTT CGG CGA AGT CGT
leu glu glu ala ile leu gly thr ile gly ala arg gln glu met val arg arg ser arg
4021/1341
GAG AGG AGC CCG TTT GGG AAT CCA GAG AAC GTG CGC TGG CGG AAG AGC GTC ACA CAC TGG
glu arg ser pro phe gly asn pro glu asn val arg trp arg lys ser val thr his trp
4081/1361
AAG CAA ACC TCA GAC CGC GTG GAC AAG ACC AAG GAT GAA ATG GAA CAC GAG GCC TTG GTG
lys gln thr ser leu asp arg val asp lys thr lys asp glu met glu his glu ala leu val
4141/1381
GAA GGG AAC CTG GCA ACC GAG GCA AGC CTA GTG GTT CTG GAC ACA CTG GAG ATC ATC GTG
glu gly asn leu ala thr glu ala ser leu val val leu asp thr leu glu ile ile val
4201/1401
CAG ACG GTG ATG CTT TCA GAA GCC CGG GAG AGC GTC TTG GGG GCA GTG CTG AAG GTT GTG
gln thr val met leu ser glu ala arg glu ser val leu gly ala val leu lys val val
4261/1421
CTG TAC AGC CTG GGC AGT GCC CAG AGT GCC CTC TTC TTG CAG CAT GGC CTG GCC ACC CAG
leu tyr ser leu gly arg leu leu arg his cys gly ser arg ile ser thr ile arg thr his
4321/1441
AGG GCC CTT GTG TCC AAG TTC CCG GAG CTG CTG TTC GAG GAG GAC ACG GAG CTG TGT GCC
arg ala leu val ser lys phe pro glu leu leu phe glu glu asp thr glu leu cys ala
4381/1461
GAC CTG TGC CTG AGG CTC CTA CGA CAC TGT GGC AGC CGC ATC AGC ACC ATC CGC ACG CAC
asp leu cys leu arg leu leu arg his cys gly ser arg ile ser thr ile arg thr his
4441/1481
GCC AGC GCC TCG CTG TAC CTG CTC ATG CGA CAG AAC TTC GAG ATC GGC CAC TTT GCC
ala ser ala ser leu tyr leu leu met arg gln asn phe glu ile gly his asn phe ala
4501/1501
CGT GTG AAG ATG CAG GTC ACC ATG TCT CTC TCG TCC CTG GTG GGG ACG ACG CAG AAC TTC
arg val lys met gln val thr met ser leu ser ser leu val gly thr thr gln asn phe
4561/1521
AGT GAA GAG CAC CTG CGA CGT TCA CTC AAA ACC ATC CTC ACC TAT GCT GAG GAG GAC ATG
ser glu glu his leu arg arg ser leu lys thr ile leu thr tyr ala glu glu asp met
4621/1541
GGG CTG CGG GAC AGC ACC TTC GCA GAG CAG GTC CAG GAC CTG ATG TTC AAC CTG CAC ATG
gly leu arg asp ser thr phe ala glu gln val gln asp leu met phe asn leu his met
4681/1561
ATC CTG ACG GAC ACG GTG AAG ATG AAG GAA CAC CAG GAG GAC CCT GAG ATG CTC ATC GAC
ile leu thr asp thr val lys met lys glu his gln glu asp pro glu met leu ile asp
4741/1581

3571/1191
TCA ATG CTT GAC TCA GAC ACA
3631/1211
AAC CCC TCT GTG GCC ATG GCC ATT GCT GGT
3691/1231
ATC TCC CAG GGG CCA CCA ACG GCT TCT CGC
3751/1251
CGG ACC TTG CTG GCG TGT GTG CTG TGG GTG
3811/1271
CGC TGG GCC ACT GAC CTG ACA CTC CCC CAG
3871/1291
TGC CTG GCT GCC TTT GAG TAC AAG GGG AAA
3931/1311
TTC AAA AAA TCT CTG GAT ATG AAG GCG CGG
3991/1331
GCT CGA CAA GAA ATG GTT CGG CGA AGT CGT
4051/1351
GTG CGC TGG CGG AAG AGC GTC ACA CAC TGG
4111/1371
AAG GAT GAA ATG GAA CAC GAG GCC TTG GTG
4171/1391
GTG GTT CTG GAC ACA CTG GAG ATC ATC GTG
4231/1411
val val leu asp thr leu glu ile ile val
4291/1431
CTC TTC TTG CAG CAT GGC CTG GCC ACC CAG
4351/1451
CTG TTC GAG GAG GAC ACG GAG CTG TGT GCC
4411/1471
leu phe glu glu asp thr glu leu cys ala
4471/1491
gly ser arg ile ser thr ile arg thr his
4531/1511
TCG TCC CTG GTG GGG ACG ACG CAG AAC TTC
4591/1531
thr ile leu thr tyr ala glu glu asp met
4651/1551
val gln asp leu met phe asn leu his met
4711/1571
CAC CAG GAG GAC CCT GAG ATG CTC ATC GAC
4771/1591
his gln glu asp pro glu met leu ile asp

CTC ATG TAC AGA ATT GCC CGG GGC TAC CAG GGC TCA CCG GAC CTT CGG CTG ACC TGG TTG
 leu met tyr arg ile ala arg gly tyr gln gly ser pro asp leu arg leu thr trp leu
 4801/1601 4831/1611
 CAG AAC ATG GCC GGG AAG CAC GCG GAG CTG GGC AAC CAC GCC GAG GCC GCC CAG TGC ATG
 gln asn met ala gly lys his ala glu leu gly asn his ala glu ala ala gln cys met
 4861/1621 4891/1631
 GTG CAC GCG GCC GCC CTC GTG GCT GAG TAC CTC GCC CTG CTC GAG GAC CAG CGC CAC CTG
 val his ala ala ala leu val ala glu tyr leu ala leu leu glu asp gln arg his leu
 4921/1641 4951/1651
 CCC GTG GGC TGC GTT TCC TTC CAG AAC ATC TCA TCC AAC GTG CTA GAG GAG TCC GCC ATC
 pro val gly cys val ser phe gln asn ile ser ser asn val leu glu glu ser ala ile
 4981/1661 5011/1671
 TCC GAC GAC ATC CTG TCG CCC GAC GAG GAG GGC TTC TGC TCC GGG AAG CAC TTC ACT GAG
 ser asp asp ile leu ser pro asp glu glu gly phe cys ser gly lys his phe thr glu
 5041/1681 5071/1691
 CTG GGG CTG GTA GGG TTG CTG GAA CAG GCA GCC GGC TAC TTC ACC ATG GGC GGG CTC TAC
 leu gly leu val gly leu leu glu gln ala ala gly tyr phe thr met gly gly leu tyr
 5101/1701 5131/1711
 GAG GCG GTG AAT GAG GTC TAC AAG AAC CTC ATC CCC ATC CTG GAA GCC CAC CGT GAC TAC
 glu ala val asn glu val tyr lys asn leu ile pro ile leu glu ala his arg asp tyr
 5161/1721 5191/1731
 AAG AAG CTG GCC GCG GTG CAC GGC AAA CTG CAG GAG GCC TTC ACC AAG ATC ATG CAC CAG
 lys lys leu ala ala val his his gly lys gln glu ala phe thr lys ile met his gln
 5221/1741 5251/1751
 AGT TCC GGC TGG GAG CGC GTG TTC GGG ACG TAT TTC CGC GTG GGC TTC TAC GGC GCC CAC
 ser ser gly trp glu arg val phe gly thr tyr phe arg val gly phe tyr gly ala his
 5281/1761 5311/1771
 TTC GGT GAC CTG GAT GAG CAG GAG TTT GTG TAC AAG GAG CCA TCG ATC ACG AAG CTG GCA
 phe gly asp leu asp glu gln glu phe val tyr lys glu pro ser ile thr lys leu ala
 5341/1781 5371/1791
 GAG ATC TCA CAC CGG CTG GAG GAG TTC TAC ACG GAG AGA TTT GGC GAC GAC GTC GTT GAG
 glu ile ser his arg leu glu glu phe tyr thr glu arg phe thr lys ile met his glu
 5401/1801 5431/1811
 ATT ATC AAA GAC TCT TAC CCT GTG GAC AAG TCC AAG CTT GAC TCA CAA AAG GCC TAC ATC
 ile ile lys asp ser tyr pro val asp lys ser lys leu asp ser gln lys ala tyr ile
 5461/1821 5491/1831
 CAG ATC ACG TAT GTG GAA CCG TAC TTT GAT ACC TAC GAG CTC AAG GAC CGG GTG ACC TAC
 gln ile thr tyr val glu pro tyr phe asp thr tyr glu leu lys asp arg val thr tyr
 5521/1841 5551/1851
 TTT GAC CGC AAC TAT GGG CTT CGC ACA TTC CTG TTC TGC ACG CCG TTC ACG CCG GAT GGG
 phe asp arg asn tyr gly leu arg thr phe leu phe cys thr pro phe thr pro asp gly
 5581/1861 5611/1871
 CGC GCA CAC GGG GAG CTG CCC GAG CAA CAC AAG CGT AAG ACG CTG CTC AGC ACC GAC CAC
 arg ala his gly glu leu pro glu gln his lys arg lys thr leu leu ser thr asp his
 5641/1881 5671/1891
 GCC TTC CCC TAC ATC AAG ACT CGC ATC CGT GTG TGC CAC CGG GAG GAG ACG GTG CTG ACG
 ala phe pro tyr ile lys thr thr arg ile arg val cys his arg glu glu thr val leu thr
 5701/1901 5731/1911
 CCA GTG GAG GTG GCC ATC GAG GAC ATG CAG AAG AAG ACA CGG GAG CTG GCC TTT GCC ACC
 pro val glu val ala ile glu asp met gln lys lys thr arg glu leu ala phe ala thr
 5761/1921 5791/1931
 GAG CAG GAC CCA CCA GAT GCT AAG ATG CTA CAG ATG GTG CTT CAG GGC TCT GTA GGG CCC
 glu gln asp pro pro asp ala lys met leu gln met val leu gln gly ser val gly pro
 5821/1941 5851/1951
 ACC GTG AAC CAG GGT CCC CTG GAG GTG GCC CAG GTG TTT TTA GCA GAG ATC CCG GAA GAC
 thr val asn gln gly pro leu glu val ala gln val phe leu ala glu ile pro glu asp
 5881/1961 5911/1971
 CCC AAG CTC TTC CGG CAT CAC AAC AAA TTG CGG CTC TGC TTC AAG GAC TTC TGC AAG AAA
 pro lys leu phe arg his his asn lys leu arg leu cys phe lys asp phe cys lys lys
 5941/1981 5971/1991
 TGT GAG GAT GCG CTG CGG AAA AAT AAG GCC CTG ATT GGG CCG GAC CAG AAG GAG val TAC CAC

cys glu asp ala leu arg lys asn lys ala leu ile gly pro asp gln lys glu tyr his
 6001/2001 6031/2011
 CGT GAG CTG GAG CGC AAC TAC TGC CGC CTG CGG GAG GCT CTG CAG CCC CTG CTT ACC CAG
 arg glu leu glu arg asn tyr cys arg leu arg glu ala leu gln pro leu leu thr gln
 6061/2021 6091/2031
 CGC CTG CCC CAG CTG ATG GCA CCC ACC CCA CCC GGC CTC AGG AAC TCC TTG AAC AGA GCA
 arg leu pro gln leu met ala pro thr pro pro gly leu arg asn ser leu asn arg ala
 6121/2041 6151/2051
 AGT TTC CGA AAG GCA GAC CTC TGA GCC CAC AAG GAC CAA AGC TGT ACC TAG AGG AAC CAG
 ser phe arg lys ala asp leu OPA
 6181/2061 6211/2071
 CAC CCG GGC CTC AGC TGT CTG TGC TGC GAG GGG AGT CTG CCC TGG TGC CCA CTG GGC TGT
 6241/2081 6271/2091
 GGG GTG ACC ACA CTG TAC TTG GGG CTG GGC CCT CTG CCC CTG TGT CCC CAT CTG TGT GCA
 6301/2101 6331/2111
 CTG ATG CTT CCT CCC TTT TTT AAT TTA AAA TGG TTT TTA TAA GCA AAA AAA AAA AAA AAA

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A. Allelic variations: single nucleotide changes (polymorphism) between CLASP-7 cDNA isoforms

Isoform	Nucleotide(s)	Consequence
1	1993	G to A; glycine to arginine
2	2136	A to G; missense
3	3166	A to G; threonine to alanine
4	3902	A to T; lysine to methionine
5	3918	C to T; missense
6	3937	A to C; lysine to glutamine
7	4002	A to C; glutamic acid to aspartic acid
8	4017	T to A; serine to arginine
9	4020	T to C; missense
10	4034-5	TT to AC; phenylalanine to tyrosine
11	4911	G to C change; missense mutation changing codon from glutamine to histidine

These differences may be found separately or together in various combination in the difference human CLASP-7 isoforms

FIG. 5

B

CLASP-7 intron/exons

Exon 63800 to 63920

GCGGGGCCGGGGCCCGGGGCGGCGGCGGGGACGCGAGGACCATGGCTGC
CTCCGAGCGCGCGCCTTCGCGCACAAAGATCAACAGGTAGTGTGGCCGCGGG
GCCCCCTCCACCTCC

Exon 72530 to 72670

CCAATGGCCCCCTCCCTATCTTTCCAGGACGGTGGCCCGAGAGGTGCGGAAG
CAGGTGTCCCGGGAACGCAGTGGCTCCCCCACTCCAGCAGGCGCTGCAGCA
GCTCCCTGGGGGTAAGTATTTGGGGGGTCCGCCCCCA

Exon 73300 to 73530

TCACAGCCACTTTGCTCCAATCCAGGTCCCACTGACTGAAGTTGTCGAGCCCC
TGGACTTIGAGGATGTACTTCTGAGCCGCCACCAGATGCTGAGCCCGGGCC
CCTCAGGACCTGGTAGAATTCACAGCTGATGACTTGGAGCTGCTGCTGCA
CCCCGGGAATGCCGGACCACGGAGCCCGGGATCCCCAAGGATGAGTGGGTTC
AGCCCCACGCCCTCTCTGCCTG

Exon 73700 to 73830

GTCTCTGTTTACCCTGATCTTTTGTGCTGCAGAAACTGGATGCCCAGGTGA
GGGCCGCGGTGGAGATGTATATTGAGGACTGGGTCAITGTCCACAGAAGGTG
AGTCTGACTTAGGGGCAGCTCAGGGG

Exon 74010 to 74190

CCTGCCAGCCCCGTTTCTGCTAGGTATCAGTACCTGAGTGCAGCATACAGC
CCCGTCACCACAGACACACAGCGGGAGCGACAGAAGGCCTCCCCCGCCAG
GTCTTTGAGCAGGATGCTTCTGGAGACGAGAGGTCCGGCCCTGAGGACTCG
TGAGGAAGCCCCTGGCTGGGGTCAC

Exon 75170 to 75450

CAGTGCTTGACATTCTCCACTGGCAGAAATGACTCCCGCGCTGGCTCGGGCTC
CCCGGAAGACACCCCTCGAAGCAGTGGTGCCTCTAGCATCTTCGACCTGAGG
AACCTGGCAGCTGACTCAITGCTGCCCTCTCTGCTAGAGCGGGCGGCCCCAG
AAGATGTGGACCGGCGCAATGAAACCTTCGACGGCAGCACCGGCCCCCGGC
CCTGCTCACCTCTACCCGGCACCTGACGAGGTGGGTGCCCTTCCAGATAT
CAGCCAACCAGCATTTACT

Exon 78100 to 78250

CCCCGCCAGCTCCCACCCCCACTCTTGGCAGGATGAAGCCGTGGAACGCTG
TAGCCGCCCAGAGCCACCCGCGAGCACTTTGGACAAAGGATCTTGGTCAAG
TGTCTGTCGCTCAAGTGAGTATACTGACATGTCTCTCTTCTTAGATG

Exon 80380 to 80500

CCCCCTCCCTCCCATTACTTGTAGGTTTCGAGATTGAAATTGAGCCCATCTTT
GGGATCTTTGGCTCTGTATGATGTGCGGGAGAAAAAGAAGGTAGGAGGCCCTT
TTTTCTCTTCTCCCTCC

Exon 80540 to 80750

GTGGTGGCCAGCTGCCTCTGGTGTCCCCAGATCTCGGAGAACTTCTACTTCG
ACCTGAACCTCGGACTCCATGAAGGGGCTGCTTCGGGCTCATGGCACCCACCC
TGCCATCTCCACCTTGGCCCGCTCTGCCATCTTCTCTGTGACCTACCCCTCACC
TGACATCTTCTGTGCATCAAGGTGCCTGCTGGGGCTGGGCAAGGGGGTGGT

Exon 82370 to 82510

GCCTCACTGGATTCACTCATCTGCCCCGCAGTTGGAGAAGGTGCTTCAGCAAG
GGGACATCAGTGAGTGCTGTGAGCCTTACATGGTGTTGAAAGAAGTGGACAC
AGCCAAGGTAAGCGTGTGAGGCTGGACTAGGGGCA

Exon 82540 to 82760

GCTGAGCTGGCAGGGGACGGGGTCTCCCCACAGAACAAAGAGAAGCTAGAG
AAGCTGCGCCTGGCGGGCCGAGCAGTTCTGCACCCGCCCTGGGCCGCTACCGCA
TGCCCTTCGCCTGGACGGCCGTGCACTTGCCCAACATCGTGAGCAGCGCTGG
GCAGCTGGACCGGACTCTGACTCGGAGGGCGGTGAGGAGGCGGGGCTAAC
AGGCTTGGGGCGGGG

Exon 82860 to 83060

CTTGGTCCCCCTTTTGTCAATTGTCATTCCCTCCCCTAGAGCGCCGGCCAGCCT
GGACAGACCCGCCCGTCGGGGGGCCCCAGGACCGGCGCAGTAGTGGGGACG
ACGCTGCAGCTTCTCTGGCTTCCGTCCAGCCACGCTAACTGTCAAACTTC
TTTAAGCAGGTGTCTACCTGGGGCCAGGGACTCTCCCACTCC

Exon 83100 to 83260

GCCAGGCTGACGGGAGTGGGTCCCATGTAGGAGGCTGAGCGACTCAGTGAC
GAGGACCTCTTCAAGTTCTGGCTGACATGAGGCGCCCGTCGTCCTGCTGCG
GCGACTACGTCCTGTGACTGGTGCGTGGCACACCCCATACACAAGAAGTATC
ACTC

Exon 84050 to 84270

GTGCAAACCGGTTCTTCCCTTCCCAGCCCAGCTCAAGATCGACATTTCTCCGG
CTCCTGAAATCCCCACTTCTGCCTCTCCCCTGAGCTGCTTCATATCAAGCCC
TACCCGGACCCCAGGGGCCGCCACCAAGGAGATTCTGGAGTTCCCCCGCC
GCGAAGTCTATGCCCCCATACCAGCTACAGGTACGGCCCTCTGGGGCCACG
TGGGCACTTGA

Exon 87940 to 88130

GCCCTGTCCCTCTGACACCCCCATCCTGCCCCCAGGAACTGCTGTACG
TGTACCCGCACAGCCTCAACTTCAGCAGCCGCCAGGGCTCCGTGCGCAACCT
TGCTGTGCGAGTGCAGTACATGACAGGCGAGGACCCAGCCAGGCTCTGCCG
GTCAGTGCTGTGCCCCAGGGAAGGGGGTAGGG

Exon 88140 to 88270

TGGGTCCCTCATGAATCCACTCTCCAGGTCATCTTTGCGCAAGTCCAGCTGCA
GTGAATTTACCCGCGAGGCCTTACACCGGTGGTCTACCATAACAAGTATGT
AGGGGGACACGTGAGGAACCTGGGGG

Exon 88470 to 88680

GCCCCAGCAGATCCCCAGCCGATTCTGCCAGGTCCCCGAGTTCTACGA
GGAGTTCAAGCTGCATCTTCCAGCCTGCGTGACAGAGAACCATCACCTGCTG
TTCACCTTCTACCATGTGAGCTGCCAGCCCCGGCCGGGCACTGCCCTGGAGAC
ACCCGTGGGCTTTACTGTGAGCCGTCCCTCCCTCCCTCCCCCTGAGCCCTCC
T

Exon 88680 to 88870

TCGTCCCCAACCTGGCCGAGACCTGACCTCCAGCCTCTCCCAGTGGATCC
CACTGTGCAGCACGGGCGCCTGAGGACCGGCCCTTCTGTCTCCCAGTGTCT
GTGGACCAACCGCCGCCAGCTATTCGGTGCTCACACCCGATGTATGTGCCCT
GGAGCTCTGCGCTGCCAATGCACTGTCCCCAG

Exon 89360 to 89530

CAGGGAGGGCTGACCAGTGCCACCTGGTGCCTCCCTCCCACAGGTGGCGCT
TCCGGGCAATGCGCTGGGTGGACGGTCACAAGGCGCTGTTCAAGTGTGGAGCTC
ACAGCCGTGTCTCTGTGCACCCCCAGGTACGGGGTGGCCGGGAACCAAGA
GTCCGCGCCTGTCTC

Exon 89660 to 89980

TTCATTCCCTGAGGCCCCACCCTGCTCACTCCACATCCCTACCCAGGACCCCT
ACCTGGACAAATTCTTACCCTGGTGACGTCTGGAGGAGGGAGCCTTCCC
ATTCCGGCTCAAGGACACTGTGCTGAGCGAGGGCAACGTGGAGCAGGAGCTG
CGGGCCAGTCTTGACGACTGCGCCTGGCCAGCCCCGAACCCCTTGTGGCCTT
CTCCACCACGTGCTGGACAAGCTCGTGCGTCTGGTCAACAGGCCCCGATC
ATCAGTGGCCAGATTGGTAAGCGAATGTGGCCTCAGACCTCAGTTTCCCCATC
CACATG

Exon 90480 to 90730

AGAGGCCCTTGGGCCCTGGAACTTGACCTCTGCTCTGCCCTGCAGTGAACCTG
GGCCGTGGAGCCTTTGAAGCAATGGCCCATGTAGTCAGCCTTGITCACCCGA
GCCTGGAGGCAGCCAGGATGCCCGCGGTCACTGCCCACAGCTGGCTGCCTA
CGTCCACTACGCCTTTCGCCCTTCTGCGCACTGAGCCAGCCTCCCGGATGGTG
AGTTTGTAGAAATCCCTGTGAGACGAGAAATATCTGGGAGAA

Exon 92870 to 93120

ATCACATCAGGTGGGTGGGTGGTTGACCCTATTCACCTCCATCCTCAGGGGCCC
CTCCAGTGACAGTGACAGGCTGCCACACTGGCCCGTGGCTCTGGTTCGCCCCG
AAGCCTCTACCTGGCGCGTTCCAAGAGCATCAGCAGCAGCAACCTGACCTC
GCCGTGGCCCCCTGGCTCTGTGGATGACGAGGTTTCCCGCATCCTGGCCAGCA
AGGTAGGGCAACGGGGGCCCTGGAATCTCCAGCCTCAGTGGT

Exon 97210 to 97390

GGCACCTCGCACTCTGTGACCCCTGCCTCTGTCCCCAGCTGCTTCACGAGGAG
CTGGCTCTGCAGTGGGTGGTGCAGCAGCAGTGCCGTACGCGAGGCCATCCTCC
AGCACGCCTGGTCTTCTTCCAGCTCATGGTGAGACCCCTCCTCCCTGCCTG
GTGGCAAGAGACCCCACTGGAG

Exon 98770 to 98990

CAAATCCCAACCACAGCCCTCTCACCCCAACCCCAAGGTGAAGAGTATGGCGC
TGCACCTGCTGCTTGGCCAGCGACTAGACACACCCCGCAAGCTGCGCTTCCC
CGGACGCTTCTGGACGACATCACTGCCTTGGTGGGCTCTGTGGGCCTGGAG
GTCATCACCCGTGTCCACAAGGTGAGAGATGCAGGGTCTCAATGTGGGAAGA
AACCTGAGGGAGG

Exon 103130 to 103340

GGGGCTGAGGTTTGGGTGTGTGGGTTGACAGGCACCTGTGTCCCCAGGATGT
GGAGCTGGCCGAGCACCTCAACGCCAGCCTGGCTTTCTTCCTCAGTGACCTTC
TGTCCCTGGTGGACCGGGGCTTTGTCTTCAGCCTGGTCCGGGGCCCACTACAAG
CAGGTAGGAAGTGGGCGTGGGCAGGCTGGGCATGGCATGGATGGAAGGCGGA
GC

Exon 103340 to 103590

CAATGTTGACATCACTGATGGCCACCCCTCTCCTGCAGGTGGCCACGCGGCTC
CAGTCGTCCCCTAATCCAGCAGCCCTGCTGACCCCTGCGCATGGAATTCACCCG
CATCCTGTGCAGCCACGAGCACTACGTGACCCTCAACCTCCCCTGCTGCCCTC
TGTACCTCCAGCCTCGCCCTCCCCCTCTGTGTCTCCACCACTCCCAGGTG
GGCTGCCTTCACTTCTGCCTCCTCTCTTTGACCTACAAC

Exon 103990 to 104220

TGACCCTTGACCGCTGGCATCCCCATTTTCCCCCACTCTGCAGAGCTCCAC
CTTCTCCAGCCAAGCCCCGGACCCCAAGGTGACCAGCATGTTTCGAACTGAGT
GGACCATTCGGGCAGCAGCACTTCTTAGCTGGGCTCCTGCTGACGGAGCTGG
CACTGGCCCTCGAACCTGAGGCTGAAGGGTGAGCAGAGCTCCTGTCTAGCCC
CAGGACAGGTGGGACAGTCCAG

Exon 104220 to 104480

GGAGCCATGTCCACCCTGTCTGTGAGCACCTCATTACCCCATAGGGCATTCTGT
TTGCACAAGAAGGCCATCAGTGCTGTGCACAGCCTGCTATGTGGCCATGACA
CTGACCCCGCTACGCCGAGGCCACTGTGAAGGCTCGTGTGGCCGAGCTGTA
CCTGCCACTGCTATCGATTGCACGGGATACCTTGCCACGGCTGCATGACTTTG
CTGGTCAGTGGGCCAGGGGAAGATGGGGTCACATGATCCAGGGACTTGGTC

Exon 108850 to 109100

ACCAAGGGTTTATCTTTCTTTCCCTCTGTCTTTCCCTGCCAGAGGGCCCAGGTC
AGCGGTCAAGACTGGCCTCAATGCTTGACTCAGACACAGAAGGCGAAGGGG
ACATTGCCGGTACCATCAACCCCTCTGTGGCCATGGCCATTGCTGGTGGCCCC
CTAGCCCTGGCTCCCGGGCCAGCATCTCCAGGGGCCACCAACGGTGAGTA
GGGAGGCTTGTCCCCATAGACATCATCCACTTTGAATGAGA

Exon 109140 to 109410

TCACATGGAGAAAATGGAAATTGACTTTGATTCTCTCTGGCCCCAGGCTTCT
CGCGCAGGCTGTGCCCTCTCTGCTGAGTCAAGCCGGACCTTGTGGCGTGTGT
GCTGTGGGTGCTGAAAAACACCGAGCCGGCGCTCCTGCAGCGCTGGGCCACT
GACCTGACACTCCCCAGCTGGGACGTCTGTTGGATTGCTGTACCTTGCCT
AGCTGCCTTTGAGTACAAGGTTTGAGGGCGTGCGCAGGAGATGATGGAGGAG
GCAGGCTA

Exon 110310 to 110530

GAAAAGAGCAGAGTCAGCCTGGAACCCAGTTCTCTGCACCCCCAGGGGAA
AAAGGCCCTTTGAACGCATCAACAGCCTCACATTCAAAAAATCTCTGGATATG
AAGGCGCGGCTAGAGGAAGCCATTCTGGGTACCATCGGAGCTCGACAAGAA
ATGGTTTCGCGGAAGTCGTGTAAGAGGGTGACATACCCACGTGTCCCATCC
CACCAGCTGCTCCCA

Exon 110770 to 110940

TGTGTTTTTACGCATCTGTGATCGTGACCCACGCGTCTCAGAGAGGAGCCCG
TTTGGGAATCCGGAGAATGTGCGCTGGCGGAAGAGCGTCACACACTGGAAGC
AAACCTCAGACCGCGTGGACAAGTAGGTGTGGCAGGAGGGTGTCTGCTGAG
TTCAGAACAGTTTG

Exon 111590 to 111770

ATCTCACCCCGAGTGGGCCCCCAAGACCTCCTTTCCCTTCCAGGACCAAGG
ATGAAATGGAACACGAGGCCCTTGTTGGAAGGGAACCTGGCAACCGAGGCAA
GCCTAGTGGTTCTGGACACACTGGAGATCATCGTGACAGGTAGGGCTTGATCC
AGCATCTGCCTTGTGCTCTGAGCCCA

Exon 111830 to 112050

ACCCTAGGCTCTAACACCTGGATTCTGACCCCTTCCCTCCAGACGGTGATG
CTTTCAGAAAGCCCGGGAGAGCGTCTTGGGGGACAGTGCTGAAGGTTGTGCTGT
ACAGCCTGGGCACTGCCAGAGTGCCCTCTTCTTGACAGATGGCCTGGCCAC
CCAGAGGGCCCTTGTGTCCAAGGTGAGCACCCTCAACAACCATGATTCTTA
GAAAAACAGTAG

Exon 112910 to 113140

AACGGGGAGGGGCTGGACAGTGTCTGTCTGGGTCCTTGGGGGCAGTTCCCGG
AGCTGCTGTTTCGAGGAGGACACGGAGCTGTGTGCCGACCTGTGCCTGAGGCT
CCTACGACACTGTGGCAGCCGCATCAGCACCATCCGCACGCACGCCAGCGCC
TCGCTGTACCTGCTCATGCGACAGAACTTCGAGATCGGCCACGTGAGTGGGG
GCTAGGAGGCATGGTCCACACATGGCTCTGGTC

Exon 114090 to 114340

TCTGAGACTCCCGGCTCCACCTCCCGCCCCCTGTCCCTGCAGAACTTTGCCCG
TGTGAAGATGCAGGTCAACATGTCTCTCTCGTCCCTGGTGGGGACGACGCAG
AACCTTCAGTGAAGAGCACCTGCGACGTTCACTCAAAACCATCCTCACCTATG
CTGAGGAGGACATGGGGCTGCGGGACAGCACCTTCGCAGAGCAGGTGACAC
CTGTGGGTCCCCGCCCCGCTCCCTTCATATAACTCCCAAC

Exon 114370 to 114550

ATGCTCTCATTGGCCCCTGGACGTTCCCCGGCTCCAGGTCCAGGACCTGATGT
TCAACCTGCACATGATCCTGACGGACACGGTGAAGATGAAGGAACACCAGG
AGGACCCTGAGATGCTCATCGACCTCATGTACAGGTGAGGTGGGCCAGCTGG
CACCTTCAGCCACGCCACGCCCA

Exon 116900 to 117170

AGGTGAGTCCCTCCTCACATCCCCCTCACCTGGACTCCAGAAATTGCCCGGG
GCTACCGGGCTCACCGGACCTTCGGGCTGACCTGGTTGCAGAACATGGCCGG
GAAACACGCGGACGTGGGCAACCACGCGGAGGCCGCCAGTGATGGTGCA
CGCGGCCGCCCTCGTGGCTGAGTACCTCGCCCTGCTCGAGGACCAGCGCCAC
CTGCCCCTGGCTGGCGATTTCCTTCCAGGTGAGTGGCCAGGGGTGGCAGGT
GGCGGACGGCA

Exon 117170 to 117410

ACGAGTGCAGTGGGACCAGGGTCTGACGCCACCTCTCCACCCCAGAACAT
CTCATCCAACGTGTAGAGGAGTCCGCCATCTCCGACGACATCCTGTCCGCC
GACGAGGAGGGCTTCTGCTCCGGGAAGCACITCACTGAGCTGGGGCTGGTAG
GGTTGCTGGAAACGGCAGCCGGCTACTTCACCATGGTGAGGCCTTGGGGACT
GGGTGCAGGAGAGGGGGCTCGGGCCAGGGAGGT

Exon 121670 to 121900

GAGAGGAAGACAGTTTGGGGAATCCTGACCCACCTCACCTCAGGGCGGGC
TCTACGAGGCGGTGAATGAGGTCTACAAGAACCTCATCCCCATCCTGGAAGC
CCACCGTGACTACAAGAAGCTGGCCGCGGTGCACGGCAAACCTGCAGGAGGC
CTTCACCAAGATCATGCACCAGGTGGGCCAGGACCCCTCCCCAGACCCA
CCCTCAGCCCCACTCCTCATCC

Exon 121910 to 122000

CCCCAGGGATCTGCTGACCTTGACCTTCTCTTCCCCACAGAGTTCCGGCTGG
GAGGTGAGTCAGCCTTGGTGGACAGCCACCTGCCTCTG

Exon 123290 to 123510

TCCAGCAGGGGCTCCCGGACAACCACACCTTTCTCACAGCCCCAGCGGT
GTTCCGGGACGTATTTCCGCGTGGGCTTCTACGGCGCCCACTTCGGTGACCTGG
ATGAGCAGGAGTTTGTGTACAAGGAGCCATCGATCACGAAGCTGGCAGAGAT
CTCACACCGGCTGGAGGCATGTCCTTGTGGTTGGGGGTGGAACGGGGCATGG
GGCTGCCTTGGG

Exon 123510 to 123633 (end clone)

GGCTGGAGTAGGGGCTGTCCCTGGGTGGCCCCGAGTCAGCCCTGTGTCTCCA
GGAGTTCTACACGGAGAGATTTTGGCGACGACGTCGTTGAGATTATCAAAAGAC
TCTAACCTGTGGACAAGTC

Human CLASP-7 promoter region , 61938 (beginning of contig) to 63888 (end of first predicted exon)

GGGCATGTGGCTCATTCTGTAATCCCGGCACTTTGGGAGGCCGAGGCGGGTGGATC
ACCTGAGGTCAGGAGCTCCAGACCAGCCTGGCCAACATGGTGAACCCCGTCTCTAC
TAAAAATACAAAAAATTAGCCAGGTGTGATGGTGGGTGCCTGTAATCCCAGCTACTC
GGGAGGCTGAGGCAGGAGAAATCGCTTGAACCTGGGAGGCAGAGGTTGCCGTGAGCC
GAGATTGTGCCATTGCACTCCAGTCTGGGCAACAAGAGCGAAATGCCACCTCAAAAT
AAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAGAGGATAA
AATGCCAGCAACCCATAGATGGGAATGAGAACAGCAGCTGCAAAGGCCCTGAGGCA
GAGCCACGGCCTTGTCTGATTCAACCTCAAATTTCTCCCTGGGGCATTTGCTGACCAGG
GAAAGAAGGGCTGTCCAGGAGGAAGGACCTGCCGGTGCAAGGCATGCAGGTGAGA
AAGGGGTGAGCTCCTCCAGAGGGGAGTGTGCGCTGGAGAATTCTCTAAAAATGCTGC
AGCAGTGCTGGGAGAGAGGCCAGTGGGGAGAGATTGAGACCATAGATTAAACCAAG
ACATCCCCACCTTCTCTTGTGTAGAGCGGCCCGAAAGTCTAGACTCCCAAACT
GGCTCACTCAGGTCCACCACTGGACCTGGGGCACATCTCCGAGCACTCCAGTGCC
TAGCCAGGCTCCTCTGACTCCCATGCTGTAGACTGGGAGCACGGACAATGCAGGCGC
TGGAGACCCTGTGAGTCACACTGAGCAAGCACCCGAACACCTCTGTGCCTCAGTTT
ACTCATCTGTAAAGGAGGAAAAACAATAATTTCTTCTGCACTGTGTGAATTGCAGGGC
CAGGCTCAATGCACATCTTAGCAATTAGACTTTTTGAGACAGGGTCTCGCTCTGTCAAC
CAGGCTGGATTGAAATGGCACAATCACAGCTCACTGCAGCCTTGACCTCCAGGCTC
AAGCGATCCTCCTCCCTCAGACTCCCAAGTAGCTGAGATTACAGGCACACACCACCA
TGCTGTGTTAATTTTGCATTTTTGTGGACACGGGGTCTCATTATGTTGCCAGGCT
GGTCTCAAACCTCTGGGCTCAAACAATCCTCTGCTTGGCCCCCACAGTGCTGGG
ATTACAGGCATGAGCCACCATGCACGGCCACGATTATACTACAGGTATGATTATA
GATACATGAACATCGTTATTGTTTTCCAGCCAGGAGTCAGAGGGCAGAAAGAGCGCC
CCCCAAACCCGGAAATCTGGGGCTACCCAGCCTGGGTCCAGCGCCTCCCTCCC
TCCCTCCCTCCTGAGCTTCAGTTTCCCCAGCCCTGCTCCTGGGGTGGTAAGACCAACC
CACTAAACCCCGGAGCCTGGGGTCCACCTAGCCCGGTCTCAGCGCCTCCCTCCC
TCCCTCCCTCCTCAGGCTCAGTTTCTCCAGCCAGCTCCAGGGTGGAAGAGCGCC
CCCGCAGCTCGGGAGTCTGGGGCACCCCCAGTCTGGGTCCAGCGCCTCCTCTCCC
TAACCTCCCTCCTCAGCTCAGTTTCCCCAGCCCTTCTCTAGGGTAGAAAGAGCGTC
CCCCAGCCCGGAGTCTGGGGCCCGCCAGCCTGGATCCGGGGCCTCCTCTCCGT
CCCCAGCTCAGTTTCCCCAGCCCCAGGACTCCAGGCGACCCCTCCGGCCTGCAGG
GGCAGCAGGAGCGGCGCGGGCCACCCGGAAGGGCCCCGCGCCGCGGGCCCCG
CCCCCGCGGCTGCCCGAGAACCGGAGGCGGCGCGCGCGGGCCGGGGCCG
GGGCGCGGCGCGGGACGCGAGGACCATGGCTGCCTCCGAGCGCGCGCCTCGC
GCACAAGATCAACAGG

FIG. 6

B

hCLASP4	TPVGF AW FW PL LKDGRITTFEQ L LPV SA NLPPGY LN LN DA ESRRQ CNV DIKWVDGAK PL LK	74
hCLASP5	TLIGYSW LP LILNERLQ TG SYCL PA LK VA LK PP PNYS MS HA EQ V LP Q NP PKI KA E AG H KG V FN	75
hCLASP3	TPG Y T W I PM LQ NG RL KT Q FC LP VS L E K PP Q AV SL PE VP --- LPQ MA W DN H KG V FN	62
hCLASP2	TVQVGSW LP L L K GR DRV TV EQ HI FPV SN L PS GH LG Y Q ELG MG HR HY G PE IKWVDG GK PLK	74
hCLASP7	TPVGFTW IP L L Q GR LR LT GF CP LP VS V DP Q PP SY SV LT PD V A ---LPQ MA W DN H KG V FN	70
hCLASP1	TPSG Y AW LP L M K HD IQ AS Q EY NI AT LS LP NY LS FQ DS AS GK H G SD SI IKWVDG GK PL FK	83

hCLASP4 FKSHLESTIYTDQLHVHKFFHHCLIQS-----GSKEVPGELIKYLKCLHAM 794
hCLASP5 IEVAVSSVHTQDNHLEKFFTLCHSLESQVTFPIRVLDQKISEMALEHKLKLSIICLNSS 715
hCLASP3 VEVAVSSIHTQDPYLDKFFALVNALDEH-LFPVIRIGDMRIMENNLENELKSSISALNSS 780
hCLASP2 ISTHLVSTVYTQDQHLNHFQYQCKTES-----GAQALGNELVLYKLSLHAM 787
hCLASP7 VELTAVSSVHPQDPYLDKFFTLVHVLEEG-AFPFRLKDTVLSEGNVEQLRASLALRLA 767
hCLASP1 VSTFVSTVNTQDPHVNAFFQECQCKREK-----MSQSPSTNFRSCKNLNVE 887
.. *:: ** ::. ** : ..

hCLASP4 EIQVMIQFLPVILMQLER-----VLTMTH-----EDDVP 824
hCLASP5 RLEFLVLFLHLVLDKLEQLSVQPMVIAGQTANFSQFAFESVVAIANSLNHNSKDLSDQHG 775
hCLASP3 QLEFVVRFLHLLDKLLVLRPPVIAGQIVNLGGSFEAMASINRLHKNLEGNHDQHG 840
hCLASP2 EQFMIAFLPTILNQLER-----VLT-RAT-----QEEVA 816
hCLASP7 SEPLVAFSHHVLDDKLVLRVIRPPIISGGIVNLGRGAFEAMAHVSVLHRSLEAAQDARG 827
hCLASP1 KIHAMSFLPIILNQLER-----VLVQNE-----EDEIT 916
.. : * : * : *

hCLASP4 INCTMV-LLHIVSKCHEEGLDS-----YLRSFIKYS-----FRPEKP 860
hCLASP5 RNCILASVYVHYFRLPEVQRDVPKSGAPTALLDPRSXYHTYGRTSAAAASSKLLQARVMSS 835
hCLASP3 RNSLLASYIHVYFRLPENTYPNSSSPG-PGGLGGSVHYATMARSAVRPASLNLRNSRSLN 899
hCLASP2 VNVTRV-IIHVVAQCHEEGLES-----HLASVVKYA-----YKAEPY 852
hCLASP7 HCPQLAAYVHYAFRLPGTEPSLPDGAPP-----VTVQAATLARGSGRPASLYLARSKSIS 883
hCLASP1 TTVTRV-LPDIIVAKCHEEQLDH-----SVQSYIKFV-----FTRAC 952
. . . :

hCLASP4 SAPAQALIH-----ETLATMIAILKQS----- 883
hCLASP5 SNPDLAGTHSADEEVKNIMSSKIADRNCRMSYYCSGSSDAPSSFA----- 882
hCLASP3 SNFDISGTPSPDDEVRSIIGSKGLDRSNSVWNTGGPKAAPWGSNPSAESTQAMDRSC 959
hCLASP2 VASZYKTVH-----ELTKSMTTILKPS----- 875
hCLASP7 SNPDLAVAPGSVDDEVSRILASKLLHEELA-LQ----- 915
hCLASP1 KE---RPVH-----EDLAKNVTGLLKS----- 972
. . . :

hCLASP4 -----ADFLSINKLLKYS-----WFFFEIIAKSM 907
hCLASP5 -----APRPASKKHFEELALQ-----MUVSTGMVKMS 910
hCLASP3 NRMSSHTETSSFLQTLTGLRPTKKLFHEELALQWVVCSSGVSRESALQQAFFFEILMKMS 1019
hCLASP2 -----ADFLTSNKKLLRYS-----WFFFDVLKMS 899
hCLASP7 -----WVVSAAVREAILQHA-----WFFFLQMKMS 942
hCLASP1 -----DSPTVKHVLKHS-----WFFFAILKMS 995
. * .. : ***

Cadherin Cleavage

hCLASP4 ATYLLEENKIKLHRCGRFPETYHHVLSLLAIIPHVTIRYAEIPDE---SRNVNYSLAS 964
hCLASP5 AQVHNMOKRDSERTRFSDREMDDITIVNVVTSEIAALLVKPQKENEQAERKMNISLAF 970
hCLASP3 VHHLYENDKLEAKRSRFFPEREMDDIAALVSTIASDIVSRFQKDTEM---VERLNTISLAF 1076
hCLASP2 AQHLIENSCKLLIRNQRFPASVYHAAETVVMIMPHITQKFGDNPEA---SKNANSLAV 956
hCLASP7 ALHLLDQKRLDTERKLFPGREFLDITALVGSVGLVITRVHKDEL---AEHLNLSLAF 999
hCLASP1 AQHLIDTNKIQLERPQRPESYQNELDNLMVMSDHWIKYKDAAEE---TRRATSVAR 1052
.. : . : * * . . . : . : . : *

hCLASP4 FLKRCLTLMDRGFFINLINDYISGFSPKDP-----KVLAEYKFEFLQTCINHEHYIPLNL 1019
hCLASP5 FLYCLLSLMDRGFVFNILIRHYCSQLSAKLSNL-----FTLISMRLFLRLCSHEHYIPLNL 1027
hCLASP3 FLNDLLSVMDRGFVSLIKSCYQVSSKLYSLNPSVLVSLRLDLRLIICSHEHYIPLNL 1136
hCLASP2 FIKRCFTFMDRGFVFKINNYISCFAPGDP-----KTLFEYKFEFLRVVCNHEHYIPLNL 1011
hCLASP7 FLSDLLSLVDRGFVSLVRAHYKQVATRLQSSPNPAALLTLRMEFTRLICSHHEHYIPLNL 1059
hCLASP1 FLKRCFTFMDRGCVFKNVNNYISMFSSGDL-----KTLQYKFDLFEVQCQHEHFIPLCL 1107
* : : : * * : . . . : . : . : *

Cadherin EC motif

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hCLASP4      ALQDN-----YETRYTAISVKNLLIKHAFDTRYGHQKQQAIAQLYLPFGVGLLENIDRL 1116
hCLASP5      ALDAQDEGIGSKVQRKAVSAIHSLLSSHDLDPRCVKPEVKVIAALYLPVGLITDLPDA 1143
hCLASP3      ILDPDAEGLIKHKKKVIMVHNSLLSSHSDSPRYSVDQIKKAVAMLYLPLIIGITMETV 1254
hCLASP2      ALQEER-----YLRLATAISVKNLLIKHSDFFDRYSRASHQARIATYLPLIFGLLINEVRI 1108
hCLASP7      ALEPFAEGAFILPVLKIASVHSLSCGHDDTPRYAEATVKVARVELYLPLISLIARDTDLP 1177
hCLASP1      ALQEDQ-----DVRHLIALVLKNIMAKHSDFFDRYEPRPKQAQIASLYMPLYGMLILDNMPIRI 1213

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hCLASP4	AGRTDLYSCA-----AMPN-S-----ASRDEFPCCGFTSPANRGSLSLTDKDTAYGS	1160
hCLASP5	-----QL-----CDFTVADTRRYRTSGSD-----	1162
hCLASP3	-----QLY-----DFETHNRQRPICLATDD-----	1276
hCLASP2	NVRDVSFPFVNAGMTVKDESLALPA-VNPLVTPQKGSGLDNLSHKLDLGAISGIASPYTT	1167
hCLASP7	-----RLH-----DFAEGPGQRSLRSLMDSLTE	1201
hCLASP1	YLKDLYPFTVNTSNQGRDRLSTNGGFOSOTAIAHKANSVDTSPKDLVNLIAAFSSIAS	1273

hCLASP4	FQ-NGHGKIKRDSRSLIPEGATGFPDQNGTGEN-----TQSSSTRSSVSQYNRILDQYE	1213
hCLASP5	-----EEQEGAGINQNVALAIGNNFNFLK-----SGIVLSSLPFYQKNMLNADT	1208
hCLASP3	-----YSESGSMISQTVMALIGTSVQPLTR-----PGSFLLTSSQGRKHTFSFAES	1324
hCLASP2	STPNISVNRNADSRGSLISTDGSNLPERNSEKSNLDDKHQSSLTGNSVVRCKDKLSQAE	1227
hCLASP7	-----GGGDIAGTINPSVAMALAGGLPAGPS-----ASISQGPPTASRAGCALSAES	1249
hCLASP1	-----TVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRLALIGSLTRFDRLDQAE	1327

hCLASP4	IRSLLMCYLYIVKQISEDTLLTYWNKVSQPELINILILLEVCLFHERYMGKRNRIARVHDA	1273
hCLASP5	TRNIMICFLWIMKGNADQSLIRKQWITDPTQLNRLLDLLFICVLCFEYKKGQSSDKVSTQ	1268
hCLASP3	RSLLILCLLNVLKNADETVLKRWFTDLISVLQNRLLDLLYCVSCFEYKGGKVFERNLSL	1384
hCLASP2	IRSLLMCLFYLYLKSMSDPALETYWNKASTLMDFFTTISEVCLHQFYQMYGKKYIARNQEG	1287
hCLASP7	SRTLTLACVNVLKNETPALLQRWATDLTLPQLGRLLDLLYCLLAAFEYKGGKVFERNLSL	1389
hCLASP1	TRSLLMCLFLHIMKTISETYLAIYQWRAPSPVEVSDFSIILDVCLQNFERYLKGKRNRIKIAA	1387

hCLASP4	WLSKHFGIDR-----	KSQTMPALNRNSGVQARLQHLSSLESS-----	1311
hCLASP5	VLQSRDVKAR-----	LEEALLRGEARGEMRRRAPGNDRPFLGNEN-----	1310
hCLASP3	TFKKSMDRAK-----	LEEALIGIGARQEMVRRSRGQLERSPGSFAFGSQ	1431
hCLASP2	LGPIVHDRKS-----	QTLPVSRNRTGMHARLQQLGSLDNS-----	1323
hCLASP7	TFKKSIDMKAR-----	LEEALIGIGARQEMVRRSERSPGFNEN-----	1350
hCLASP1	AFKFVSTONGNTLKGSNFSCOTSGLLAAOHMSTSRHEGHKHSOTLP	IIRGKN-----	1442

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hCLASP4      -----FTLNHSSSTTTEADIFHQALLEGNTATEVSLTVLDTISFFQKPTQLL 1359
hCLASP5      ---LRWKKEQTHWRQANEKLKDLKTELQDQALISNGATEAHLIILDMQENIQAASS-ALD 1368
hCLASP3      ENLNRWKDMTHWRQNETKDLKDSRAIEHEALIDGNLATEANLIILDTIEIVQTVS-VTE 1389
hCLASP2      -----LTFNHSGHSDADVLHGSLEANIATEVCLTALDITSLTEFLAFKNQLL 1371
hCLASP7      ---VRNRKSVTHWQTSRDVRDTKIEHEALVEGNLATEASVLVLDITIEIVQTVS-LSE 1407
hCLASP1      ---ALSNPKLLQMLDMTMTSNSNEIDIVHVTDEANIEAGCGLTILDVLSLETQTHQRQLQ 1500

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	ITAM	ITAM	
hCLASP4	EQFGTENVKIIQDSKVNAKELDPK	YAHIQVITVKEVYFDDKELTERKTEFERNHNISRFV	1799
hCLASP5	KQGAEFVEVIKDSFPVKTKLPDN	KAYIQITVEVEYFD EYEMKDRVTYFEKNFNLRRFM	1810
hCLASP3	ERFGEVUVEIKDSNPVGVKCLDPN	KAYIQITVEVEYFD EYEMKDRVTYFDKNYNLRFM	1932
hCLASP2	DKFGSENVKMIQDSKVNPKDLDPK	YAYIQVITVKEVYFDDKELQERKTEFERNHNRFFV	1770
hCLASP7	ERFGDGVUVEIKDSFPVVKKCLDSK	KAYIQITVEVEYFD EYELKDRVTYFDKNYGLRFLF	1851
hCLASP1	DKFGANVKIIQDSKVNPKDLDPK	YAYIQVITVKEVYFEFEKEIEDRKDTFEMMHNIRFV	1792

hCLASP4	FEAPYTLSGKKQGCIEEQCKRRTILTNSNFFYVKGRIPINCEQQINLKPIDGATDEIKD	1859
hCLASP5	YTFPTLEGRPRGELHEQYRRNTLTMTMAHFYIKTRISVIQKEEFLTPIEVAIDEMKK	1870
hCLASP3	YCTPFLTDGRAHGEELHEQFKRRTILTSHAFYIKTRWNTHKEELTPIEVAIDEMSK	1992
hCLASP2	FEMPFTQTGKRQGVVEEQCKRRTILTAHCFYVKGRIPVMYQHHTDLNPIEVAIDEMSK	1830
hCLASP7	FCTPFTPDGRAGHELVEQHKRRLLTSDHAFYIKTRIRVCHREETLTPVEVAIDEMKD	1911
hCLASP1	FETPFTLSGKKGHGVAEQCKRRTILTSHFFYVKGRIOVISOSSTLNPVEVAIDEMSR	2032

hCLASP4	KTAE LQKLCSSTVDVMIQLQLKLQGVSVVQVNVAGPLAYARAF LND SQASKYPKKVSE LK	1919
hCLASP5	KTYLQLAVAINHQEPDPDKMLQMVQLG SVGTAVNQGFLEVAQVFLAEIPADPKLYRHHNKL	1930
hCLASP3	KTQELAFATINQDDPDKMLQMVQLG SVGTGVNQGFLEVAQVFLSEIPSDPKLYRHHNKL	2052
hCLASP2	KVAEELRQLCSSAEVMIKLQLKLQGVSVVQVNVAGPLAYARAF LDDTNTKRYPNKVKLLK	1890
hCLASP7	KTRELA FATQEPDPDKMLQMVQLG SVGTGVNQGFLEVAQVFLAEIPEDPKLYRHHNKL	1971
hCLASP1	KVSELNQLCTMEEVDMISLQLKLQGVSVVKVNVAGPMAYARAFLEETNAKKYPDNQVKLLK	2092

hCLASP4	DMFKRFIQACSFALELNERLIKEDQVEYHEGLKSNFRDMVKLESDI	IHEQILQEDTMHSP	1979
hCLASP5	LCFKEFMTRGCEAVEKNKRLITADQREYQELKKNYNKLENLRPM	IERKIPELYKPIFR	1990
hCLASP3	LCFKFDITKCEDALRNKNSLIGVQREYQRELGKSSP		2090
hCLASP2	EVFRFVEACGQALAVNRNLIKEDQVEYQEMKANYREMAKLESIT	IMHQICPLEKTS	1949
hCLASP7	LCFKDFCKCEALRNKNALIGPDQVEYHRELRERNYCRREALQPI	LTQRLPQMAPPT	2030
hCLASP1	EIFRQFADACGALDVNRNLIKEDQVEYELRSYKMDLSELSTWNE	QITGRDDLSKR	2152

	PDZ ligand	
hCLASP4	WMSNTLHVFCIAISGTSDDRGYGSPFYAEV	2008
hCLASP5	VESQKRDSFHRSSFRCCKETQLSQGS----	2015
hCLASP3	-----	
hCLASP2	VLPNSLHI FNAISGTPPTSTMVHGHTSSV	1980
hCLASP7	-----PGLRNSLRNASFRAKDL-----	2047
hCLASP1	GDVQDCTRHLISKATPALPTVISISSAEVI	2180